

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 17:47:10 ; Search time 16 Seconds
(without alignments)
461.450 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKSLVIRNLDQVL.....LKKEDELGDRSIMFTVQNEQ 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	811	99.9	193	IL18_HUMAN	Q14116 homo sapien
2	659	81.2	193	IL18_HORSE	Q9xsg7 equus caball
3	654	80.5	193	IL18_BOVIN	Q9tu73 bos taurus
4	637	78.4	192	IL18_PIG	O19073 sus scrofa
5	613	75.5	193	IL18_CANPA	Q9xsr0 canis famil
6	515	63.4	192	IL18_MOUSE	P70380 mus musculu
7	514.5	63.4	194	IL18_RAT	P97636 rattus norv
8	178.5	22.0	196	IL18_CHICK	Q8qf98 gallus gall
9	88	10.8	4705	FAT2_DROME	Q9vw71 drosophila
10	81.5	10.0	270	IL1A_PIG	P18430 sus scrofa
11	81	10.0	267	IL1A_RABIT	P04822 oryctolagus
12	80	9.9	1449	DPO3_CLOPE	Q8xjr3 clostroidium
13	77.5	9.5	674	MUTL_CLOPE	Q8x186 clostroidium
14	76.5	9.4	270	IL1A_HORSE	Q28385 equus caball
15	75.5	9.3	192	OASB_MOUSE	Q60856 mus musculu
16	75.5	9.3	1036	Y414_MYCCE	P47653 mycoplasma
17	75.5	9.3	1663	CO3_MOUSE	P01027 mus musculu
18	74.5	9.2	1228	ECM_HUMAN	Q3201 homo sapien
19	74	9.1	467	M3K8_MOUSE	Q07174 mus musculu
20	74	9.1	467	M3K8_RAT	Q63562 rattus norv
21	74	9.1	1772	MSP1_PLAYO	P13828 plasmodium
22	73	9.0	270	IL1A_FELCA	Q46613 felis alive
23	73	9.0	418	SVS_UREPA	Q9pr38 ureaplasma
24	73	9.0	426	YXCX_ASTIO	P88151 astasia lon
25	72.5	8.9	313	COL4_ARATH	Q9m9b3 arabidopsis
26	72.5	8.9	412	UVSE_CLOPE	Q8xp33 clostroidium
27	71.5	8.8	268	IL1A_BOVIN	P08831 bos taurus
28	71.5	8.8	467	M3K8_HUMAN	P41279 homo sapien
29	71.5	8.8	527	RAG2_HUMAN	P55895 homo sapien
30	71	8.7	700	NONA_DROME	Q04047 drosophila
31	70.5	8.7	245	KDSB_FUSNBI	Q8ria8 fusobacteri
32	70.5	8.7	268	IL1A_CAPHI	P79161 capra hircu
33	70.5	8.7	644	YGM4_YEAST	P53129 saccharomyc

RESULT 1

ID	IL18_HUMAN	STANDARD;	PRT;	193 AA.
AC	Q14116; 075599;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)			
DE	(IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).			
GN	IL18 OR ICIF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE=Liver;			
RX	MEDLINE=96247646; PubMed=8666798;			
RA	Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,			
RA	Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,			
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.;			
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression			
RT	in Escherichia coli, and studies on the biologic activities of the			
RT	protein.;"			
RL	J. Immunol. 156:4274-4279 (1996).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RA	Yong D., Guixin D., Lihua H., Haitao W.;			
RT	"Cloning and sequencing of the cDNA for precursor hIL-18.;"			
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RA	Liu J., Peng X., Yuan J., Qiang B.;			
RT	"Cloning of human interleukin 18 cDNA.;"			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			

ALIGNMENTS

ID	IL18_HUMAN	STANDARD;	PRT;	193 AA.
AC	Q14116; 075599;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)			
DE	(IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).			
GN	IL18 OR ICIF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE=Liver;			
RX	MEDLINE=96247646; PubMed=8666798;			
RA	Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,			
RA	Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,			
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.;			
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression			
RT	in Escherichia coli, and studies on the biologic activities of the			
RT	protein.;"			
RL	J. Immunol. 156:4274-4279 (1996).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
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RT	"Cloning and sequencing of the cDNA for precursor hIL-18.;"			
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RT	"Cloning of human interleukin 18 cDNA.;"			
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RL	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SEQUENCE OF 2-193 FROM N.A.
TISSUE=peripheral blood;
Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC
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EMBL; D49950; BAA08706.1; -;
EMBL; AF077611; AAC27787.1; -;
EMBL; AY044641; AAK95950.1; -;
EMBL; BC007007; AAH07007.1; -;
EMBL; BC007461; AAH07461.1; -;
EMBL; U90434; AAB50010.1; -;
Genew; HGNC:5986; IL18.
MIM; 600953; -;
DR GO: GO:0005576; C:cytoplasmic; TAS.
DR GO: GO:0016506; F:apoptosis activator activity; ISS.
DR GO: GO:004871; F:signal transducer activity; TAS.
DR GO: GO:0001525; P:angiogenesis; IDA.
DR GO: GO:0007267; P:cell-cell signaling; TAS.
DR GO: GO:0042033; P:chemokine biosynthesis; TAS.
DR GO: GO:0042253; P:granulocyte macrophage colony-stimulating f. . . ; TAS.
DR GO: GO:0006955; P:immune response; TAS.
DR GO: GO:0008625; P:induction of apoptosis via death domain rec. . . ; ISS.
DR GO: GO:0042095; P:interferon-gamma biosynthesis; TAS.
DR GO: GO:0042231; P:interleukin-13 biosynthesis; TAS.
DR GO: GO:0042094; P:interleukin-2 biosynthesis; TAS.
DR GO: GO:0042104; P:positive regulation of activated T-cell pro. . . ; IDA.
DR GO: GO:0030155; P:regulation of cell adhesion; IDA.
DR GO: GO:0030431; P:sleep; ISS.
DR GO: GO:0042092; P:T-helper 2 type immune response; TAS.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.

FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CONFLICT 66 66 F -> L (IN REF. 2).
FT CONFLICT 86 86 S -> R (IN REF. 2).
FT CONFLICT 191 191 N -> S (IN REF. 2).
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 99.9%; Score 811; DB 1; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.9e-69;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNPRTFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNPRTFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISKLSCENKIISFKEMNPPDNINKDKSDIIFQRSVPGHDKNQPFESSY 120
DB 97 AVTISVKCEKISKLSCENKIISFKEMNPPDNINKDKSDIIFQRSVPGHDKNQPFESSY 156
QY 121 EGYFLACEKERDLFKLLKKEDELGRSIFMTVQNEED 157
DB 157 EGYFLACEKERDLFKLLKKEDELGRSIFMTVQNEED 193

RESULT 2
IL18_HORSE
ID IL18 HORSE STANDARD; PRT; 193 AA.
AC Q9XSG7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIP.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
SEQUENCE FROM N.A.
RA Nicolson L., Fenna-Goncalves M.N., Keanie J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC

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EMBL; Y11131; CAA72013.1; -;
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAC CRC64;

Query Match 81.2%; Score 659; DB 1; Length 193;
Best Local Similarity 77.7%; Pred. No. 1.2e-54;
Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNPRTFIISMYKDSQPRGM 60
DB 37 YFGRLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCTDNPAPQVFIIMYKDSLTRGL 96
QY 61 AVTISVKCEKISKLSCENKIISFKEMNPPDNINKDKSDIIFQRSVPGHDKNQPFESSY 120
DB 97 AVTISVKCEKISKLSCENKIISFKEMNPPDNINKDKSDIIFQRSVPGHDKNQPFESSY 156
QY 121 EGYFLACEKERDLFKLLKKEDELGRSIFMTVQNEED 157
DB 157 KGYFLACEKERDLFKLLKKEDELGRSIFMTVQNEED 193

RESULT 3
IL18_BOVIN
ID IL18 BOVIN STANDARD; PRT; 193 AA.
AC Q9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=20012648; PubMed=10547157;
RA Shoda L.K., Zarlenga D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RL 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC
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CC
DR EMBL; AF124789; AAF08686.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.5%; Score 654; DB 1; Length 193;
Best Local Similarity 77.1%; Pred. No. 3.6e-54;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YFGKLESLVIRNLNDQVLFIDQGNRPFLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 HFGKLEPKLSIIRNLNDQVLFINGQNPVFEDMPDSCSDNAPQTVFIYWKDSLTRL 96

Qy 61 AVTISVCKEKISXLSCKENKIISPKENPPDNIKDTKSDIIFQFORSVPGHDKMOPFESSY 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 AVTISVQCKKMTLSCKNKITLSPKEMSPDNIDEGNDIIFQFORSVPGHDDKIQFESSLY 156

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
157 KGYFLACKKENDLFLKILKKEDEGDRSIMFTVQNK 193

RESULT 4
IL18_PIG STANDARD; PRT; 192 AA.
AC O19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.

```

```

RC TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849;
RA Fournout S., Dozois C.M., Yerville M., Pinton P., Fairbrother J.M.,
RT Oswald E., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT pig interleukin-18.";
RL Immunogenetics 51:358-365(2000).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
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CC
DR EMBL; U68701; AAC18415.1; -
DR EMBL; Y11132; CAA72014.1; -
DR EMBL; AB010003; BAA24135.1; -
DR EMBL; AF191088; AAF1200.1; -
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35 BY SIMILARITY.
FT CHAIN 36 192 INTERLEUKIN-18.
SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.4%; Score 637; DB 1; Length 192;
Best Local Similarity 75.2%; Pred. No. 1.4e-52;
Matches 118; Conservative 24; Mismatches 15; Indels 0; Gaps 0;

Qy 1 YFGKLESLVIRNLNDQVLFIDQGNRPFLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
36 YFGKLEPKLSIIRNLNDQVLFINGQNPVFEDMPDSCSDNAPQTVFIYWKDSLTRL 95

Qy 61 AVTISVCKEKISXLSCKENKIISPKENPPDNIKDTKSDIIFQFORSVPGHDKMOPFESSY 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 AVTISVQCKKMTLSCKNKITLSPKEMSPDNIDEGNDIIFQFORSVPGHDDKIQFESSLY 155

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
156 KGYFLACKKENDLFLKILKKEDEGDRSIMFTVQNK 192

RESULT 5
IL18_CANFA STANDARD; PRT; 193 AA.
AC Q9XSR0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99309818; PubMed=10380699;

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RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;
RT "Cloning, sequencing, and characterization of dog interleukin-18.";
RL Immunogenetics 49:541-543 (1999).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
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CC -----
DR EMBL; Y11133; CAAT2015.1; -
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0016506; F:apoptosis activator activity; IEI.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. . . ; IEI.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. . . ; ISS.
KW Cytokine.
FT PROPEP 1 36
FT CHAIN 37 193
FT INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22037 MW; 0D973E386F461F25 CRC64;

Query Match 75.5%; Score 613; DB 1; Length 193;
Best Local Similarity 73.7%; Pred. No. 2.4e-50;
Matches 115; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIIISMYKDSQPRGM 60
DB 37 YFGKLEPKLSIIRNLNDQVLFVNEGNQPVFEDMPDSDCTDNAPHTIFIIYMYKDSLTRLG 96
QY 61 AVTISVKCKISXLSCKNIISFKENPPDNKDTKSDIIFQSVPGHDKNMQFESSSY 120
DB 97 AVTISVKYKMTSLCKNKTISFKQSPDPSINDEGNDIIFQSVPGHDKNMQFESSY 156
QY 121 EGYFLACEKERDLFKILKKEDELGRSINFTVQNE 156
DB 157 KGHFLACKENDLFKILKDKENGKSVNFTVQNK 192

RESULT 6
IL18 MOUSE
ID IL18 MOUSE STANDARD; PRT; 192 AA.
AC P70350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96061009; PubMed=7477296;
RA Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,
RA Tanimoto T., Torio K., Okura T., Nukada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RL Nature 378:88-91 (1995).
RN [2]
RP SEQUENCE OF 1-191 FROM N.A.

RC STRAIN=NOD; TISSUE=Pancreas;
RX MEDLINE=97174346; PubMed=9022080;
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474 (1997).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
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CC -----
DR EMBL; D49949; BAA08705.1; -
DR EMBL; U66244; ABA49753.1; -
DR MGD; MGI:107936; IL18.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0016506; F:apoptosis activator activity; TAS.
DR GO; GO:0001525; F:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. . . ; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. . . ; TAS.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IMP.
DR GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
DR GO; GO:0042094; P:interleukin-2 biosynthesis; ISS.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. . . ; ISS.
DR GO; GO:0030155; P:regulation of cell adhesion; ISS.
DR GO; GO:0030431; P:sleep; ISS.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192
FT INTERLEUKIN-18.
FT CONFLICT 183 185
SQ SEQUENCE 192 AA; 22135 MW; 8FD938473874D63 CRC64;

Query Match 63.4%; Score 515; DB 1; Length 192;
Best Local Similarity 64.9%; Pred. No. 3.4e-41;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGLKESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIIISMYKDSQPRGWA 61
DB 37 FGLHCTTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASAPQTRLIYMYKDSVRGUA 95
QY 62 VTISVKCKISXLSCKNIISFKENPPDNKDTKSDIIFQSVPGHDKNMQFESSSY 121
DB 96 VTLVKDKSKMSTLCKNKTISFEENPPENIDDIQSDLIFFQKRVFGH-NKMEFESSLYE 154
QY 122 GYFLACEKERDLFKILKKEDELGRSINFTVQNE 155
DB 155 GHFLACQEDDAPKILKDKENGKSVNFTVQNK 188

RESULT 7
IL18 RAT
ID IL18 RAT STANDARD; PRT; 194 AA.
AC P97636; O88749; P97637;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).

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Qy 121 EGYFLACEKERDLFKLILKKKDEBLGRSINFTVQN 155
    ||:||||:| ||:||||:| ||:||||:| ||:||||:|
Db 156 EGHFLACQKEDDAFKLVLRKKGDKSVNFTLTN 190

RESULT 8
IL18_CHICK
ID IL18_CHICK STANDARD; PRT; 196 AA.
AC O8QF08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18).
GN IL18.
GC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RA Rothwell L., Buerstedde J.M., Kaiser P.;
RT "Cloning and characterisation of chicken interleukin-18.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS (By similarity).
CC -I- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -I- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
EMBL; AJ276025; CAC81652.1; -
DR DR
KW Cytokine.
FT PROPEP
FT CHAIN 1 29 POTENTIAL.
FT CHAIN 30 196 INTERLEUKIN-18.
SQ SEQUENCE 196 AA; 22787 MW; 4947DECECCB92414 CRC64;

Query Match 22.0%; Score 178.5; DB 1; Length 196;
Best Local similarity 34.3%; Pred. No. 9e-10;
Matches 60; Conservative 26; Mismatches 68; Indels 21; Gaps

Qy 1 YFGKLSKL-----SVIRNLNDVLFIDOG-NRPLNDVMTDSDCRONAPRTIIS
Db 20 YFELSCDAFCDKTKTRFRNVNSQLVVRPDLNVAAPEDVTDQEVGSGS-GMYFDIHC

Qy 52 YKDSQPRG-MAVTISYKCEKIXLSCEK-----IISFKEMPNPDNIKOTKSDIIFFOR
Db 79 YKTTASARMPAVFSQVEDKSYMCCEHGMVVPRFGEVVPKDPG-ESNIIFFKTKT

Qy 106 VPCHDNK-MQFSSSYEGYFLACEKRDILFKLILKK---EDELGDRSINFTVONE 156
Db 138 FTSCSSKAPKFYSYEQGMFLAFEEBDSLRKILKLPREDEVDETTKFPVTSHNE 192

RESULT 9
FAT2_DROME
ID FAT2_DROME STANDARD; PRT; 4705 AA.
AC Q9W71; Q95S51;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative fat-like cadherin-related tumor suppressor homolog
DE precursor.
GN FAT2 OR CG7749.
OS Drosophila melanogaster (Fruit fly).

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FT DOMAIN 3084 3185 CADHERIN 29.
FT DOMAIN 3186 3289 CADHERIN 30.
FT DOMAIN 3290 3394 CADHERIN 31.
FT DOMAIN 3395 3499 CADHERIN 32.
FT DOMAIN 3500 3604 CADHERIN 33.
FT DOMAIN 3605 3712 CADHERIN 34.
FT DOMAIN 3819 3879 EGF-LIKE 1.
FT DOMAIN 3881 3919 EGF-LIKE 2.
FT DOMAIN 3937 4121 LAMININ G-LIKE.
FT DOMAIN 4129 4166 EGF-LIKE 3.
FT DOMAIN 4168 4205 EGF-LIKE 4.
FT DOMAIN 4243 4279 EGF-LIKE 5.
FT DISULFID 3823 3835 POTENTIAL.
FT DISULFID 3830 3867 POTENTIAL.
FT DISULFID 3869 3878 POTENTIAL.
FT DISULFID 3885 3896 POTENTIAL.
FT DISULFID 3890 3907 POTENTIAL.
FT DISULFID 3909 3918 POTENTIAL.
FT DISULFID 4133 4144 POTENTIAL.
FT DISULFID 4138 4154 POTENTIAL.
FT DISULFID 4156 4165 POTENTIAL.
FT DISULFID 4172 4183 POTENTIAL.
FT DISULFID 4177 4193 POTENTIAL.
FT DISULFID 4195 4204 POTENTIAL.
FT DISULFID 4247 4258 POTENTIAL.
FT DISULFID 4252 4267 POTENTIAL.
FT DISULFID 4269 4278 POTENTIAL.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 779 779 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 843 843 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1106 1106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1198 1198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1312 1312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1439 1439 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1473 1473 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1511 1511 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 3962 3962 G -> E (IN REF. 3; AAL28503).
SQ SEQUENCE 4705 AA; 524564 MW; 6D387A489D2C33DE CRC64;

Query Match 10.8%; Score 88; DB 1; Length 4705;
Best Local Similarity 23.6%; Pred. No. 11;
Matches 38; Conservative 25; Mismatches 56; Indels 42; Gaps 7;

QY " 32 DWTSDCDNDNAPRTIFLIISWY-----KDSQPRGMATISVKCEKISXLSCEKNIISF--KE 85
Db 2124 DISVLVDVNDNCP--LFVNMPPYATVSIIDPKG---TIIMQVKAIDLDSAENGVEVYELKK 2178

QY 86 MNPPDNIKDTSIDIIFFORSVPGHDKMQPFESSSYEGYFLACEKERDL----- 133
Db 2179 NGELFKLDRKSGELSIKHQVGEHNRNVELTVAAVDGAIPTCCSSAPLOVKVIDRSMVPV 2238

QY 134 ---FKLIKKED-----ELGDRSIMFTVQNE 156
Db 2239 EKQFTVSVKEDVEMYSALSVSIAESPLG-RSLIVTISSE 2278

RESULT 10
ILIA_PIG STANDARD; PRT; 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN ILIA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=90332454; PubMed=2377484;
RA Maliszewski C.R., Renshaw B.R., Schoenborn M.A., Urban J.F.,
BAker P.E.;
RT "porcine IL-1 alpha cDNA nucleotide sequence.";
RL Nucleic Acids Res. 18:4282-4282(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Huetner M.J., Scamurra R.W., Murtaugh M.P., Molitor T.W.;
RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases
CC -I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -I- SUBUNIT: Monomer.
CC -I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -I- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -I- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC -----
CC EMBL; X52731; CAA36945.1; -
CC EMBL; M86730; AAA73198.1; -
CC PIR; I46620; I46620.
CC PIR; S10532; S10532.
CC HSSP; P01583; LITA.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC Pfam; PF02394; IL1_propep; 1.
CC SMART; SM00125; IL1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 89 89 N -> I (IN REF. 2).
FT CONFLICT 242 242 F -> L (IN REF. 2).
FT CONFLICT 255 255 P -> R (IN REF. 2).
SQ SEQUENCE 270 AA; 30788 MW; 567BF2B0EF6389 CRC64;

Query Match 10.0%; Score 81.5; DB 1; Length 270;
Best Local Similarity 22.7%; Pred. No. 1.5;
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;

QY 8 KLSVIRNLNDQVLFDIQGNRLPFEDMTD-----SCDRDNAPRTI-FIISMYKDSQPRGMAY 62
Db 123 KYNFMRVINHQCILNDARNQSIIRDPSGQYLMAAVLNNLDBAVKFDMAAYTSDNDSQLPV 182

QY 63 TISVKEKISXLSCE--KIISPKEM-NPPDNIKDTSIDIIFFORSVPGHDKMQPFESS 119
Db 183 TLRLS-ETRLFVSAQNEDEPVLKELPPTKTIKDETSLLFFWEK-----HGNMDFKSA 237

QY 120 YEGYFLACEKER 131
Db 238 HPKLFIAIATQEK 249

RESULT 11
ILIA_RABIT

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ID IL1A RABIT STANDARD; PRT; 267 AA.
AC P04822;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Legomorphia; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85297782; PubMed=2994016;
RA Furutani Y., Norake M., Yamayoshi M., Yamagishi J., Nomura H.,
RA Ohue M., Furuta R., Fukui T., Yamada M., Nakamura S.;
RT "Cloning and characterization of the cDNAs for human and rabbit
RT interleukin-1 precursor."
RL Nucleic Acids Res. 13:5869-5882(1985).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: Monomer.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: Belongs to the IL-1 family.
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-----
EMBL; X02852; CAA26605.1; -
DR HSPSP; P01583; IITA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 267 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 64 64 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 267 AA; 620533FD1FA4822 CRC64;
Query Match 10.0%; Score 81; DB 1; Length 267;
Best Local Similarity 25.2%; Pred. No. 1.6;
Matches 32; Conservative 27; Mismatches 56; Indels 12; Gaps 5;
QY 12 IRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNDAPRTI-----FIISMYKDSQPRGMVITISV 66
DB 127 LRIIKQEFNLNDALNSQLVSDTSDOYLRAAPLQNLGDAVKFDGVTMTSDSILPVLTRI 186
QY 67 KCKSIKSLSCEN--KIISPKEM-NPPDNINKDTKSDIIFQFORSVPGHDKNMQPFSSSYEGY 123
DB 187 SQTPLE-FVSAQNDEPVLVKEMPETPRITDSSDILFFWET---QGNKNYFKSAANPOL 242
QY 124 FLACEKE 130
DB 243 FIATKPE 249
-----
RESULT 12
DPO3 CLOPE STANDARD; PRT; 1449 AA.
AC Q8XJR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III polC-type (EC 2.7.7.7) (PolIII).
GN POLC-OR CPE1691.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=13 / Type A;
RX MEDLINE=121664373; PubMed=11792842;
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- FUNCTION: Required for replicative DNA synthesis. This DNA
CC polymerase also exhibits 3' to 5' exonuclease activity (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. POLC
CC SUBFAMILY.
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EMBL; AF003191; BAB81397.1; -
DR HAMAP; MF_00356; -; 1.
DR InterPro; IPR006054; DnaQ.
DR InterPro; IPR006055; Exonuclease.
DR InterPro; IPR004013; PHP_C.
DR InterPro; IPR003141; PHP_N.
DR InterPro; IPR006308; PolC_gram_pos.
DR Pfam; PF02811; PHP_C; 1.
DR Pfam; PF02811; PHP_C; 1.
DR Pfam; PF02231; PHP_N; 1.
DR SMART; SM00479; EXOIII; 1.
DR SMART; SM00481; POLIIIAC; 1.
DR TIGRFAMs; TIGR00573; dnaq; 1.
DR TIGRFAMs; TIGR01405; polC_Gram_pos; 1.
DR Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW Nuclease; Exonuclease; Complete proteome.
FT DOMAIN 435 598 EXONUCLEASE.
SQ SEQUENCE 1449 AA; 163627 MW; AE24E2CE7D372B85 CRC64;
Query Match 9.9%; Score 80; DB 1; Length 1449;
Best Local Similarity 27.2%; Pred. No. 15;
Matches 43; Conservative 21; Mismatches 52; Indels 42; Gaps 10;
QY 15 LNDQVLFIDQGNRPFLFEDMTDSDC---RDNAPRTIIFISMYKDSQPRGMVITISVCKEKI 71
DB 1196 LNNQAQYFKEGYTTL-----KDCIATRDD---INVLYMYKDLPPK-TAFTIMEKVRG 1244
QY 72 SXLSCENKIISPKEMNPPD-NITKDTKSDIIFQFORSVPGHD-----NKMOPFSS 118
DB 1245 KGLSEDEAL-NREKNVPDVIYIESCKIKYMPK---GHAVAYVMVAIVYKVIYPEA 1300
QY 119 SYEGYF-----LACEKEDLFKLILKKEDELGD 146

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Db 1301 YTTTFTVRADDFDADLICKGE-EAIKAKWEELNSIGN 1337
RESULT 13
MUTL_CLOPE STANDARD; PRT; 674 AA.
AC Q8XL86;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA mismatch repair protein mutL.
GN MUTL OR CPE1156
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -!- FUNCTION: This protein is involved in the repair of mismatches in
CC DNA. It is required for dam-dependent methyl-directed DNA mismatch
CC repair. May act as a "molecular matchmaker", a protein that
CC promotes the formation of a stable complex between two or more
CC DNA-binding proteins in an ATP-dependent manner without itself
CC being part of a final effector complex (By similarity).
CC -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEX FAMILY.
CC
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CC
CC EMBL; AP003189; BAB80862.1; -
CC HAMAP; MF_00149; -; 1.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR002099; DNA_mis_repair.
CC Pfam; PF01119; DNA_mis_repair; 1.
CC Pfam; PF03518; HATPase_c; 1.
CC SMART; SM00387; HATPase_c; 1.
CC TIGRFAMs; TIGR00585; mutL; 1.
CC PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
CC DNA repair; Complete proteome.
CC SEQUENCE 674 AA; 77205 MW; 2380566BB4500A3D CRC64;
Query Match 9.5%; Score 77.5; DB 1; Length 674;
Best Local Similarity 25.9%; Pred. No. 10;
Matches 30; Conservative 15; Mismatches 40; Indels 31; Gaps 5;
QY 17 DQVLFIDQGNRLFE-----DMTSDCR-----DNAPRTFIISMYKDSQPRGMA 61
Db 547 EYLYDE-NKEIFKAGKISDFGDSIRIEBVPYFLDKLNPTLITSMNNLNKMGVTG 605
QY 62 VTISVKCKISKLSCSE-----NKISFKEM-----NPPDNKOTKSDIIEF 102
Db 606 ETVEKYNKIASMSCRAAVKANDVLSILEMENLIEDLYINDPFPCHGRPTIIEF 661
RESULT 14
ILIA_HORSE
ID ILIA_HORSE STANDARD; PRT; 270 AA.
AC Q28385; O77743;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
DE IL1A.
DE Equus caballus (Horse).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96131982; PubMed=8578682;
RA Kato H., Ohashi T., Nakamura N., Nishimura Y., Watarai T., Goitsuoka R.,
RA Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of equine interleukin-1 alpha and -beta cDNAs.";
RL Vet. Immunol. Immunopathol. 48:221-231(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285941; PubMed=9622738;
RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT "Cloning of equine interleukin-1 alpha and equine interleukin-1 beta
RT and determination of their full-length cDNA sequences.";
RL Am. J. Vet. Res. 59:704-711(1998).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC (BY SIMILARITY).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC
CC EMBL; D42146; BAA07717.1; -
CC EMBL; U92480; AAC39255.1; -
CC HSPF; P01583; IL1A.
CC InterPro; IPR003502; IL1_propep.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC Pfam; PF02394; IL1_propep; 1.
CC SMART; SM00125; IL1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
CC Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112 BY SIMILARITY.
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 141 141 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 110 110 R -> K (IN REF. 2).
FT CONFLICT 150 150 G -> V (IN REF. 2).
SQ SEQUENCE 270 AA; 30806 MW; 381859713754DB90 CRC64;
Query Match 9.4%; Score 76.5; DB 1; Length 270;
Best Local Similarity 22.3%; Pred. No. 4.4;
Matches 29; Conservative 28; Mismatches 62; Indels 11; Gaps 4;
QY 7 SKLSVIRNLNDQVLFIDQGNRLPFEDMTSDCRDNAPRTI-----FIISMYKDSQPRGMA 61
Db 122 TKYNFMRIVNHQCTLNDALNQSVIRDTSGQYLATAALNNLNDVAVKFDGAVTSEDSQLP 181
QY 62 VTISV-KCEKISXLSCKENKISFKEM-NPPDNKOTKSDIIEFORSVPGHKNKQPFESS 119
Db 182 VTLRIKTRLFVSAQNEDEPVLKEMPDPPTKINDETNLLFFWER----HGSKNYFKSVA 237
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Search completed: December 12, 2003, 17:52:55
Job time : 17 secs.

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OASB_MOUSE STANDARD; PRT; 192 AA.
ID OASB_MOUSE AC Q00856;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 2-5'-oligodeoxylate synthetase 1B (EC 2.7.7.-) ((2-5')oligo(A)
DE synthetase 1b) (2-5A synthetase 1B) (Fragment).
DE OAS1B OR OIAS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=91232962; PubMed=1709495;
RA Rutherford M.N., Kumar A., Nissim A., Chebath J., Williams B.R.G.;
RT "The murine 2-5A synthetase locus: three distinct transcripts from two
RT linked genes."
RL Nucleic Acids Res. 19:1917-1924 (1991).
CC -1- FUNCTION: THE 2-5A SYSTEM (THE OAS, 2-5A, AND RNASE L) MAY PLAY A
CC ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL
CC GROWTH, DIFFERENTIATION, AND APOPTOSIS.
CC -1- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP
CC into PPP(A2;P5'A)N oligomers, which activate the latent RNASE L
CC that, when activated, cleaves single-stranded RNAs.
CC -1- INDUCTION: By interferons.
CC -1- SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.
CC
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CC
CC EMBL; X55982; CAA39455.1; --
CC PR; S15661; S15661.
CC MGD; MGI:197430; Oasib.
CC GO; GO:0003800; F:antiviral response protein activity; IDA.
CC InterPro; IPR006117; 25A_SYNTH_2.
CC InterPro; IPR006116; 25A_synth_UB.
CC InterPro; IPR001201; PAP_25A_CORE.
CC PROSITE; PS00832; 25A_SYNTH_1; PARTIAL.
CC PROSITE; PS00833; 25A_SYNTH_2; PARTIAL.
CC PROSITE; PS0152; 25A_SYNTH_3; 1.
CC RNA-binding; Transferase; Nucleotidyltransferase;
CC Interferon induction.
CC NON_TER 1
CC FT NON_TER 192 192
CC SEQUENCE 192 AA; 21936 MW; 4E1C01BEF9024F46 CRC64;

Query Match 9.3%; Score 75.5; DB 1; Length 192;
Best Local Similarity 21.3%; Pred. No. 3.6;
Matches 42; Conservative 24; Mismatches 50; Indels 65; Gaps 9;

QY 3 GKLESKLSVTRN-----LNQVLFIDGGRPLFPEDMTDSDCRNAPRTFIIMYKD 54
DB 11 GRSDALVLPNNLTSFDQLNQGVLLKIKQLCEVQHERRC----- 54
QY 55 SQPRGMVTVSVKCEKISLSCENKILISFKEMPNPDNIKDTKSDII----- 100
DB 55 -----GVTFEVLHSLSPNSRLSFK-LSAPDLLKEVDFVLPAYDLLHLNLKK 103
QY 101 -----FFQR---SVP-GHDNRNQVFESSYGYFLACE---KERDLFKLI-----LKKEDELG 145

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1	798	98.3	193	4	Q96KJ8	Q96KJ8 homo sapien
2	792	97.5	193	6	Q9BG15	Q9BG15 macaca mufa
3	654	80.5	178	6	Q9MZL8	Q9MZL8 bos taurus
4	648	79.8	193	6	Q9GL09	Q9GL09 ovnis aries
5	634	78.1	192	6	Q9SM33	Q9SM33 felis silve
6	626	77.1	192	6	Q9N1P7	Q9N1P7 aus scrofa
7	441	54.3	196	11	Q9IZ66	Q9IZ66 sigmodon hi
8	313	38.5	45	6	Q9SL87	Q9SL87 canis famil
9	204	25.1	84	6	Q9NQ49	Q9NQ49 homo sapien
10	193	23.8	211	13	Q98SQ1	Q98SQ1 anas platyr
11	184.5	22.7	198	13	Q8AV26	Q8AV26 meleagris g
12	182.5	22.5	198	13	Q9I8D2	Q9I8D2 gallus gall
13	86.5	10.7	376	11	Q8K4E7	Q8K4E7 mus musculu
14	86.5	10.7	376	11	Q8K4E6	Q8K4E6 mus musculu
15	85	10.5	352	11	Q8JZN4	Q8JZN4 mus musculu
16	85	10.5	381	3	Q43031	Q43031 schizosacch

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RESULT 2
Q9BGIS PRELIMINARY; PRT; 193 AA.
AC Q9BG15; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Interleukin-18.
GN IL18.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2129850; PubMed=11331040;
RA Glavendon L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
RT Simian Immunodeficiency Virus Does Not Result In Increased Viral
RT Replication.";
RL J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AAK13416.1; -
SQ SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;

Query Match 97.5%; Score 792; DB 6; Length 193;
Best Local Similarity 95.5%; Pred. No. 2e-70; Indels 0; Gaps 0;
Matches 150; Conservative 5; Mismatches 2;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIINMYKDSQPRGM 96
QY 61 AVTISVKCEKISKLSKSCENKIISFKEMNPPDNKDKSDIIFQORSVPGHDKNKQFESSY 120
DB 97 AVAISVKCEKISTLSCENKIISFKEMNPPDNKDKSDIIFQORSVPGHDKNKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 3
Q9MZL8 PRELIMINARY; PRT; 178 AA.
AC Q9MZU8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-18 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, Liver, and Blood;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrli M., Bolin C.A.;
RT "Cloning of bovine interleukin-18, expression in Escherichia coli, and
RT characterization of the biologic activities of the recombinant
RT cytokine.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF173175; AAF89833.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1
FT NON_TER 178
SQ SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match 80.5%; Score 654; DB 6; Length 178;
Best Local Similarity 77.1%; Pred. No. 7.7e-57;

Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 22 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIINMYKDSLTRGL 81
QY 61 AVTISVKCEKISKLSKSCENKIISFKEMNPPDNKDKSDIIFQORSVPGHDKNKQFESSY 120
DB 82 AVTISVQCKKMTSLSCENKIISFKEMNPPDNIDNEESDIIFQORSVPGHDKKIQFESSLY 141
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 142 KGYFLACKKENDLFKLILKQDDNRDKSVNFTVQNNQ 178

RESULT 4
Q9GL09 PRELIMINARY; PRT; 193 AA.
AC Q9GL09;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-18 (IGIF).
GN IL-18.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RT "Cloning of ovine interleukin 18 cDNA ";
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401033; CAC09326.2; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCD0A329062EF18C CRC64;

Query Match 79.8%; Score 648; DB 6; Length 193;
Best Local Similarity 77.7%; Pred. No. 3.3e-56;
Matches 122; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIINMYKDSLTRGL 96
QY 61 AVTISVKCEKISKLSKSCENKIISFKEMNPPDNKDKSDIIFQORSVPGHDKNKQFESSY 120
DB 97 AVTISVQCKKMTSLSCENKIISFKEMNPPDNIDNEESDIIFQORSVPGHDKKIQFESSLY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 KGYFLACKKENDLFKLILKQDDNRDKSVNFTVQNNK 193

RESULT 5
Q9SM33 PRELIMINARY; PRT; 192 AA.
AC Q9SM33;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interferon-gamma inducing factor.
GN IGIF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;
RT "Nucleotide sequence of feline IGIF cDNA (provisional).";

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RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; Y13923; CAC42918.1; -.

SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 78.1%; Score 634; DB 6; Length 192;

Best Local Similarity 76.4%; Pred. No. 7.9e-55;

Matches 120; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

Db 36 YFGKLEHLKLSIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSLTRGL 95

Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQFQSVPGHDNMQFESSY 120

Db 96 AVTISVYKTKMTSLSCNKIISFKEMSPESINDEGNDIIFQFQSVPGHDNMQFESSLY 155

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Db 156 KGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKN 192

RESULT 6

Q9N1P7

ID Q9N1P7 PRELIMINARY; PRT; 192 AA.

AC Q9N1P7;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Interleukin-18.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=20356335; PubMed=10901174;

RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;

RT "Cloning, sequencing, and expression of porcine interleukin-18 in

RT Escherichia coli.,"

RL Mol. Cells 10:343-347 (2000).

DR EMBL; AF196949; AAF35169.1; -.

DR InterPro; IPR000975; Interleukin_1.

DR SMART; SM00125; IL1; 1.

SQ SEQUENCE 192 AA; 21969 MW; A51EB7A4E221A16D CRC64;

Query Match 77.1%; Score 626; DB 6; Length 192;

Best Local Similarity 73.9%; Pred. No. 4.9e-54;

Matches 116; Conservative 25; Mismatches 16; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

Db 36 YFGKLEPKLSIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSLTRGL 95

Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQFQSVPGHDNMQFESSY 120

Db 96 AVTISVQCKKSTLSCNKIISFKEMSPDNIDEGNDIIFQFQSVPGHDNMQFESSLY 155

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Db 156 KGYFLACEKERDLFKLILKKEDELGDRSIMFTVQKN 192

RESULT 7

Q91266

ID Q91266 PRELIMINARY; PRT; 196 AA.

AC Q91266;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Interleukin 18.

OS Sigmodon hispidus (Hispid cotton rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1] SEQUENCE FROM N.A.
RP Blanco J.C., Platneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.,"
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059406; AAL26703.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 196 AA; 22545 MW; E27CSBDC397F951C CRC64;

Query Match 54.3%; Score 441; DB 11; Length 196;

Best Local Similarity 59.4%; Pred. No. 9.4e-36;

Matches 92; Conservative 24; Mismatches 37; Indels 2; Gaps 2;

Qy 2 FKGLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

Db 39 PFKESSTAVIRNMNDVLPIDREKSPVFEDMPDADQKANEATRLIIMYKTDNPGGL 98

Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQFQSVPGHDNMQFESSY 120

Db 99 PVTLSVRDRTMTSLSCNKIISFEEDMPDPLBIDGKSDLIFFQFQSVPGH-NMKFESSLH 157

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVON 155

Db 158 EGFFLACERDGSFLKILKKDENWDTSIIFTVTN 192

RESULT 8

Q95LE7

ID Q95LE7 PRELIMINARY; PRT; 84 AA.

AC Q95LE7;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE IL-18 (Fragment).

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;

RT "Semi-quantification of canine cytokine expression by one tube RT-PCR."

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF327900; AAL26920.1; -.

FT NON_TER 1

FT NON_TER 84

SQ SEQUENCE 84 AA; 9568 MW; 19BD9E27F336774B CRC64;

Query Match 38.5%; Score 313; DB 6; Length 84;

Best Local Similarity 74.7%; Pred. No. 1.6e-23;

Matches 59; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

Db 5 YFGKLEPKLSIRNLNDQVLFVNEGNQVPFEDMPDSDCTDNAPRTIFIIMYKDSLTRGL 64

Qy 61 AVTISVKCEKISXLSKCNK 79

Db 65 AVTISVKYKTMSTLSCNK 83

RESULT 9

Q9NQ49

ID Q9NQ49 PRELIMINARY; PRT; 45 AA.

AC Q9NQ49;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Interleukin-18 (Fragment).
GN IL-18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Farhan A.J., Pravica V., Hutchinson I.V.;
RT "Identification of Human Interleukin-18 gene polymorphisms.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295724; CAC01436.1; -.
FT NON_TER 1
FT NON_TER 45
FT NON_TER 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.1%; Score 204; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 4.7e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCR 39
Db 7 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCR 45

RESULT 10
ID Q98SQ1 PRELIMINARY; PRT; 211 AA.
AC Q98SQ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Interleukin-18 (Fragment).
GN IL-18.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF336122; AAK26322.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 211 AA; 24541 MW; CA6FC6358211B2B CRC64;

Query Match 23.8%; Score 193; DB 13; Length 211;
Best Local Similarity 36.5%; Pred. No. 3.2e-11;
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSOP-RG 59
Db 43 FSKEKTLHRLNRVNSQLVVRPDLNVAAPFDVTDQEMKSGGWN-FCMHCYKTTTPSAG 101

QY 60 MAVTISVKCE-KISXLSCEKNK-----IISFKEMNPPDNIKDKSDIIFQFORSVPGHDK-M 113
Db 102 MPVAFSVRVEDKSYVMCCBEHGKMWVRFGEVPEKIDPG-ESNMIFFKKTFTSYSSKAF 160

QY 114 QPSSSYEGYFLACEKRDLFKLILKK---EDELGDRS-IMFTVQNE 156
Db 161 KFYSLRGMFLAFEEEDSLRKLILKLKLPREDEVDETTKILTSHNE 207

RESULT 11
ID Q9AV26 PRELIMINARY; PRT; 198 AA.
AC Q9AV26;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Interleukin-18 precursor (Fragment).
GN IL-18.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaiser P.;
RT "Turkey and chicken interleukin-18 (IL18) share high sequence
RT identity, but have different polyadenylation sites in their 3' UTR.";
RL Dev. Comp. Immunol. 26:681-687(2002).
DR EMBL; AJ312000; CAC83483.1; -.
FT Signal.
FT NON_TER 1
FT NON_TER 28
FT SIGNAL <1
FT CHAIN 29 198 INTERLEUKIN-18.
FT CHAIN 29 198
SQ SEQUENCE 198 AA; 22967 MW; ALD450BC7207BFAD CRC64;

Query Match 22.7%; Score 184.5; DB 13; Length 198;
Best Local Similarity 34.9%; Pred. No. 2.1e-10;
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSOP-RG 59
Db 31 FCKEKTIKLFRVNSQLVVRPDLNVAAPFDVTDQEVKSGS-GMYFDIHCYKTTAPSAG 89

QY 60 MAVTISVKCEKISXLSCEKNK-----IISFKEMNPPDNIKDKSDIIFQFORSVPGHDK-M 113
Db 90 MPVAFSVQVEDKSYVMCCBEHGKMWVRFGEVPEKIDPG-ESNMIFFKKTFTSCSKAF 148

QY 114 QPSSSYEGYFLACEKRDLFKLILKK---EDELGDRS-IMFTVQNE 156
Db 149 KFEYSLEQGMFLAFEEEDSLRKLILKLKLPREDEVDETTKFVTSRNE 194

RESULT 12
ID Q918D2 PRELIMINARY; PRT; 198 AA.
AC Q918D2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 18.
GN IL-18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,
RA Kaspers B., Weining K.C.;
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883 (2000).
DR EMBL; AJ277865; CAB96214.1; -.
FT CHAIN 30 198 INTERLEUKIN 18.
FT CHAIN 30 198
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;
Best Local Similarity 36.8%; Pred. No. 3.2e-10;
Matches 57; Conservative 25; Mismatches 60; Indels 13; Gaps 7;

QY 13 RNILNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSOP-RGMVATISVKCEK 70
Db 42 RNVNSQLVVRPDLNVAAPFDVTDQEVKSGS-GMYFDIHCYKTTAPSAGMPVAFSQQVED 100

QY 71 ISKLSCEKNK-----IISFKEMNPPDNIKDKSDIIFQFORSVPGHDK-MQFESSSYEGYF 124
```

RA Brinton M.A.;

RT "Positional cloning of the murine flavivirus resistance gene.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:9322-9327(2002).

DR ENBL; AF418009; AAM47549.1; -;

DR MGD; MGI:97430; Oaslb.

DR InterPro; IPR006117; 25A_SYNTH_2.

DR InterPro; IPR006116; 25A_synth_UB.

DR InterPro; IPR001201; PAP_25A_core.

DR PROSITE; PS00833; 25A_SYNTH_2; 1.

DR PROSITE; PS0152; 25A_SYNTH_3; 1.

SEQ SEQUENCE 376 AA; 43842 MW; 5807F6EE436FCA26 CRC64;

Query Match 10.7%; Score 86.5; DB 11; Length 376;

Best Local Similarity 23.3%; Pred. No. 2;

Matches 40; Conservative 28; Mismatches 65; Indels 39; Gaps 7

Qy 5 LESKLSVIRNLNDQVLFIDQGNRPLFPEDMTSDCDRDNAPRTIFITISMYKDSQPRGMVTTI 64

Db 59 VVGKCTALKGRSDADLVFLNLTYPFDQLNQ-----QGVLIKEIKQLYEVOHERRF 111

Qy 65 SVKCEKISXLSCEKNIIISFKEMNPPDNIKOTKSDII-----FFQ--- 103

Db 112 GVKFEVQSLRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLKPNQQFYANLI 170

Qy 104 --RSVPHDNMQPSSSYGYFLACE--KERDLFKLI-----LKKEDELGD 146

Db 171 SGRTPPGKEGLSICFMGLRKRYFLNCRPTKLRLIRLVTHWYQLCKE-KLGD 221

RESULT 15

Q8JUN4 PRELIMINARY; PRT; 252 AA.

ID Q8JUN4

AC Q8JUN4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE 2'-5' oligoadenylate synthetase 1B (2'-5'-oligoadenylate synthetase 1).

DE OAS1A OR OAS1B OR OAS1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_taxid=10090;

ON [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H/He;

RX MEDLINE=22103633; PubMed=12080145;

RA Perylysin A.A., Scherblk S.V., Zhulin I.B., Stockman B.M., Li Y., Brinton M.A.;

RT "Positional cloning of the murine flavivirus resistance gene.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:9322-9327(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RX MEDLINE=22177231; PubMed=12186974;

RA Mashimo T., Lucas M., Simon-Chazottes D., Frenkiel M.P., Montagutelli X., Ceccaldi P.E., Deubel V., Guenet J.L., Despres P.;

RT "A nonsense mutation in the gene encoding 2'-5'-oligoadenylate synthetase/L1 isoform is associated with West Nile virus susceptibility in laboratory mice.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:11311-11316(2002).

RN ENBL; AF418004; AAM47544.1; -;

DR ENBL; AF466822; AAM97603.1; -;

DR MGD; MGI:2180860; Oasla.

DR MGD; MGI:97430; Oaslb.

DR InterPro; IPR006116; 25A_synth_UB.

DR InterPro; IPR001201; PAP_25A_core.

DR PROSITE; PS0152; 25A_SYNTH_3; 1.

SEQ SEQUENCE 252 AA; 28812 MW; 552108B5041006CD CRC64;

Query Match 10.5%; Score 85; DB 11; Length 252;

Best Local Similarity 23.1%; Pred. No. 1.8;

Matches 42; Conservative 25; Mismatches 49; Indels 66; Gaps 8


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Qy 3 GKLESKLSVIRN-----LNDQVLFIDQGNRELFEDMTDSDCRDNAPRTIFIISMYKD 54
Db 68 GRSDADLVVFINLNTSFEDQLNQGVLIKEIKQICEVQHERRC----- 111
Qy 55 SQPRGMAVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDII----- 100
Db 112 -----GVKPEVHSLRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLIK 160
Qy 101 -----FFQ-----RSVPGHDNKMQFESSSYEGYFLACE--KERDLFKLI-----LKKED 144
Db 161 PNQOFYANLISGRTPPGKEGKLSICFMGLQKIFLNCRPTKIKRLIRLVTHWYQCKE-KL 219
Qy 145 GD 146
Db 220 GD 221
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Search completed: December 12, 2003, 17:53:42
Job time : 35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 17:46:35 ; Search time 42 Seconds
(without alignments)
593.335 Million cell updates/sec

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Perfect score: 812
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Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	19 AAW77077	Human interleukin
2	811	99.9	157	21 AAY57570	Human interleukin
3	811	99.9	157	22 AAE06661	Human interleukin
4	811	99.9	157	22 AAG65294	Human interleukin
5	811	99.9	157	22 AAG65351	Human interleukin
6	811	99.9	157	22 ABB04389	Human IL-18. Homo
7	811	99.9	157	23 AAE16954	Human active inter
8	811	99.9	157	23 AAE17134	Human IL-18 protei
9	811	99.9	157	24 ABG73359	Human wild-type ma

10	811	99.9	158	21 AAY85167	Human interleukin-
11	811	99.9	180	19 AAW48959	Wild-type human in
12	811	99.9	193	18 AAW22047	Interferon gamma i
13	811	99.9	193	19 AAW46592	Amino acid sequenc
14	811	99.9	193	22 AAB30541	A human IL-18 with
15	811	99.9	193	22 AAG63830	Amino acid sequenc
16	811	99.9	193	23 AAE16953	Human precursor in
17	811	99.9	233	23 AAE16959	Ubiquitin-human in
18	811	99.9	536	23 AAE16957	Human pro-IL-18/ca
19	811	99.9	588	23 AAE16958	Human pro-IL-18/ca
20	811	99.9	1048	23 AAE16960	Ubiquitin-human in
21	810	99.8	157	17 AAR99564	Human interferon-g
22	810	99.8	157	17 AAR99558	Human mature inter
23	810	99.8	157	18 AAW15701	Interferon-gamma i
24	810	99.8	157	18 AAW24258	Human protein for
25	810	99.8	157	19 AAW77158	Human interleukin-
26	810	99.8	157	19 AAW63810	Human IL-18 protei
27	810	99.8	157	19 AAW37741	IFN-gamma inducing
28	810	99.8	157	19 AAW52176	Interferon-gamma i
29	810	99.8	157	20 AAY39799	Interleukin-18 rec
30	810	99.8	157	21 AAY44597	Human interleukin-
31	810	99.8	157	21 AAY53904	Sequence of a matu
32	810	99.8	157	22 AAB82408	Human interleukin-
33	810	99.8	193	17 AAR99560	Human interferon-g
34	810	99.8	193	19 AAW37740	Interferon-gamma i
35	810	99.8	193	19 AAW52172	Interleukin-gamma i
36	810	99.8	193	19 AAW47429	Interferon-gamma p
37	810	99.8	193	21 AAY53908	Amino acid sequenc
38	810	99.8	193	22 AAB82409	Human interleukin-
39	808	99.5	193	19 AAW77082	Interleukin 18 act
40	807	99.4	157	24 ABG73367	Human mature inter
41	807	99.4	193	24 ABG73366	Human precursor in
42	805	99.1	157	24 ABG73363	Human mature inter
43	805	99.1	157	24 ABG73364	Human mature inter
44	805	99.1	193	24 ABG73360	Human precursor in
45	805	99.1	193	24 ABG73361	Human precursor in

ALIGNMENTS

RESULT 1

AAW77077
ID AAW77077 standard; peptide; 157 AA.

XX AAW77077;

AC AAW77077;

XX 16-NOV-1998 (first entry)

DT Human interleukin 18.

DE Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;

KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;

KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.

XX Homo sapiens.

OS Homo sapiens.

PN EP861663-A2.

XX 02-SEP-1998.

XX 24-FEB-1998; 98EP-0301352.

XX 25-FEB-1997; 97JP-0055468.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

XX WPI; 1998-448964/39.

XX N-PSDB; AAW48226.

PT Use of interleukin-18 to inhibit osteoclast formation - in treatment

PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
PT osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
PT primary hyperthyroidism and osteoporosis
XX Claim 4; Page 18; 56pp; English.
XX
CC Interleukin-18 (IL-18) or a functional equivalent can be used for
CC inhibition of osteoclast formation. IL-18 is used for treating or
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
CC osteoporosis.
XX
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 2
AAV57570
ID AAY57570 standard; protein; 157 AA.
XX
AC AAY57570;
XX
DT 06-MAR-2000 (first entry)
XX
DE Human interleukin 18 protein sequence SEQ ID NO:1.
XX
DE Human; interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;
KW interferon-gamma-inducing factor; growth inhibition; cytostatic.
XX
OS Homo sapiens.
XX
PN WO9959565-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US11160.
XX
PR 21-MAY-1998; 98US-0086560.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Johnson RK;
XX
DR WPI; 2000-062368/05.
XX
XX New polypeptides, useful for preparation of composition for preventing
PT and/or treating cancer by inhibiting tumor growth
XX
PS Claim 1; Page 49-50; 53pp; English.

XX The present sequence represents human interleukin 18 (IL-18). The
CC present invention describes a compound comprising human or murine IL-18
CC in combination with a chemotherapeutic agent (I). Also described are:
CC (1) a method of preventing and/or treating cancer in a mammal comprising
CC the administration of a cancer inhibiting amount of (I) comprising the
CC IL-18 protein and the chemotherapeutic agent and optionally a
CC pharmaceutically acceptable carrier; and (2) a method of inhibiting the

CC growth of tumour cells in a mammal sensitive to a composition comprising
CC human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
CC optionally a pharmaceutically acceptable carrier), comprising
CC administering to a mammal afflicted with the tumour cells an effective
CC tumour cell growth inhibiting amount of (I). The IL-18 protein in
CC conjunction with a chemotherapeutic agent is useful in a method for
CC preventing and/or treating cancer in mammals by inhibiting the growth
CC of tumours or cancerous cells in mammals.
XX
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 21; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 3
AAE06661
ID AAE06661 standard; Protein; 157 AA.
XX
AC AAE06661;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human interleukin-18 (IL-18) protein.
XX
KW Human; interleukin-18; IL-18; virucide; hepatotropic; fever;
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS Homo sapiens.
XX
PN WO200157219-A2.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US03285.
XX
PR 02-FEB-2000; 2000US-0179638.
XX
PA (SCHE) SCHERING CORP.
XX
PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
XX WPI; 2001-488886/53.
XX
DR WPI; 2001-488886/53.
XX
PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT polypeptide useful for treating conditions exhibiting abnormal
PT expression of interleukin such as immunological disorders, tumor and
PT allergy
XX
PS Disclosure; Fig 1; 103pp; English.

XX The invention relates to recombinant antigenic interleukin-1 like
CC molecules and their corresponding nucleic acid sequences, designated
CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC abnormal expression of the interleukin such as immunological disorders,
CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary

CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
 CC HIV). The invention also relates to methods of using the composition
 CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
 CC utilities. IL-1delta is used as an immunogen for the production of
 CC antisera or antibodies specific, e.g., capable of distinguishing between
 CC IL-1 family members and an IL-1delta, for the interleukin or its
 CC fragment. The purified interleukin is used as a reagent to detect any
 CC antibodies generated in response to the presence of elevated levels of
 CC expression, or immunological disorders which lead to antibody production
 CC to the endogenous cytokine. The invention also contemplates the use of
 CC competitive drug screening assays. The present sequence is human
 CC interleukin-1gamma (IL-1gamma) protein related to the invention.
 XX
 SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 22; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 YFGKLESKLSVIRNLNDQVLPIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 Db 1 YFGKLESKLSVIRNLNDQVLPIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 Qy 61 AVTISVCKEKISLSCENKIISPKEMNPPDNIKOTKSDIIFQRSVPGHNDNMQFESSY 120
 Db 61 AVTISVCKEKISLSCENKIISPKEMNPPDNIKOTKSDIIFQRSVPGHNDNMQFESSY 120
 Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 4
 AAG65294
 ID AAG65294 standard; protein; 157 AA.
 XX
 AC AAG65294;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nontropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 FN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI; 2001-550020/61.
 XX
 Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 9; 91pp; English.
 XX
 The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The

CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein fragment.
 XX
 SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 22; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 YFGKLESKLSVIRNLNDQVLPIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 Db 1 YFGKLESKLSVIRNLNDQVLPIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
 Qy 61 AVTISVCKEKISLSCENKIISPKEMNPPDNIKOTKSDIIFQRSVPGHNDNMQFESSY 120
 Db 61 AVTISVCKEKISLSCENKIISPKEMNPPDNIKOTKSDIIFQRSVPGHNDNMQFESSY 120
 Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5
 AAG65351
 ID AAG65351 standard; protein; 157 AA.
 XX
 AC AAG65351;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nontropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 FN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI; 2001-550020/61.
 XX
 Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 14; 91pp; English.
 XX
 The invention provides isolated antibodies, or antigen-binding portions,

CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents a human IL-18 protein fragment.
XX
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 22; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKNQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKNQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 6
ID ABB04389 standard; protein; 157 AA.
XX ABB04389;
XX ABB04389;
DT 21-MAY-2002 (first entry)
XX Human IL-18.
DE Human; IL-18; interleukin-18; cancer.
KW Homo sapiens.
OS CN1326992-A.
PN 19-DEC-2001.
XX 07-JUN-2000; 2000CN-0107993.
XX 07-JUN-2000; 2000CN-0107993.
PR (SHUA-) SHUANGU PHARM CO LTD BEIJING.
PA Xu M, Wang Y, Huang X;
XX WPI; 2002-217571/28.
DR N-PSDB; ABL41315.
XX Gene cloning, product preparation and use of Chinese interleukin-18
PT subtype (53 Arg IL-18), useful for treating of cancer and other disease
PT Claim 1; Page 7 (Disclosure); 8pp; Chinese.
XX The invention relates to the preparation of recombinant human
CC interleukin-18 for treating of cancer and other disease.
XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 23; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKNQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKNQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 7
ID AAE16954 standard; Protein; 157 AA.
XX AAE16954;
AC AAE16954;
XX 18-APR-2002 (first entry)
DT Human active interleukin-18 (IL-18) protein.
DE Human; interleukin-18; IL-18; caspase; interferon gamma; IFN-gamma;
XX immunocompetent.
KW Homo sapiens.
OS WO200198455-A2.
PN 27-DEC-2001.
PD 11-JUN-2001; 2001WO-US18804.
XX 15-JUN-2000; 2000US-211832P.
PR 10-AUG-2000; 2000US-224128P.
PR 20-JAN-2001; 2001US-264923P.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Johanson KO, Kirkpatrick RB, Shatzman AR, Ho YS, Mcdevitt P;
PI WPI; 2002-139786/18.

XX Activation of precursor polypeptide e.g. interleukin-18 polypeptide
PT useful for inducing interferon-gamma production, comprises contacting
PT or co-expressing caspase 4 or caspase 5 with precursor polypeptide -
XX Claim 9; Fig 3; 64pp; English.
XX The invention relates to a method for the in vitro activation of human
CC precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The
CC method comprises contacting precursor IL-18 with an activating enzyme
CC such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family
CC of cysteine proteases that include interleukin-beta converting enzyme
CC (ICE), which preferentially cleave substrates containing a protease
CC activation motif. The methods are useful for producing physiologically
CC active polypeptide e.g. active IL-18 polypeptide. The active IL-18
CC polypeptide has an activity of inducing the production of interferon
CC (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a
CC biologically active substance for stimulating the production of IFN-gamma
CC from KG-1 (human myelomonocytic cell line) cells. The present sequence
CC is human active IL-18 protein.
XX Sequence 157 AA;
SQ Query Match 99.9%; Score 811; DB 23; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.2e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKNQMPESSSY 120
DB 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKNQMPESSSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 8
AAE17134
ID AAE17134 standard; Protein; 157 AA.
XX AC AAE17134;
XX DT 22-APR-2002 (first entry)
XX DE Human IL-18 protein.
XX OS Homo sapiens.
XX KW Human; viral disease; IL-18; interferon-gamma-inducing factor; IGIF; HSV; influenza virus; human immunodeficiency virus; HIV; herpes simplex virus; hepatitis A virus; HAV; hepatitis B virus; HBV; human papillomavirus; HPV; hepatitis C virus; HCV.
XX OS Homo sapiens.
XX PN WO200193898-A1.
XX PD 13-DEC-2001.
XX PF 01-JUN-2001; 2001WO-US17924.
XX PR 02-JUN-2000; 2000US-208869P.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PI Esser KM, Rosenberg M, Tal-Singer R, Woodnutt G, Chisari FV;
XX PT WPI; 2002-154554/20.
XX DR Treatment of disease caused by e.g. influenza virus comprises administration of composition containing polypeptide, having identity of amino acid sequences -
XX PS Claim 1; Fig 1; 41pp; English.
XX CC The invention relates to a method for treating viral diseases with IL-18, also known as interferon-gamma-inducing factor (IGIF) and IL-18 combinations. The method involves administering a composition comprising IL-18 and IL-18 in combination with other agents. The method is used for treating diseases caused by viruses such as influenza virus, human immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis A virus (HAV), hepatitis B virus (HBV), human papillomavirus (HPV) and hepatitis C virus (HCV). The present sequence is human IL-18 protein.
XX SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 23; Length 157;
Best Local Similarity 99.4%; Pred. NO. 8.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKNQMPESSSY 120

DB 61 AVTISVKCEKISTLSCEKNKIIISPKEMNPPDNIKOTKSDIIFQRSVPGHDKNQMPESSSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 9
ABG73359
ID ABG73359 standard; Protein; 157 AA.
XX AC ABG73359;
XX DT 13-MAY-2003 (first entry)
XX DE Human wild-type mature interleukin-18 (IL-18).
XX KW Human; human interleukin-18; IL-18; IL-18 binding protein; IL-18BP; T helper type I response; Th1 response; cancer; viral disease; microbial infection; tumour immunotherapy; adjuvant; DNA vaccination; graft versus tumour therapy; neutralisation; cytostatic; virucide; antimicrobial.
XX OS Homo sapiens.
XX PN US2002169291-A1.
XX PD 14-NOV-2002.
XX PF 08-MAR-2002; 2002US-0094153.
XX PR 08-MAR-2001; 2001US-274327P.
XX PA (DINA/) DINARELLO C.
XX PI (KIMS/) KIM S H.
XX PI Dinarello C, Kim SH;
XX DR WPI; 2003-298731/29.
XX DR N-PSDB; ABX11788.
XX PT Novel interleukin-18 mutant polypeptide useful in the treatment of cancer and viral disease, has mutations in amino acid residues which are involved in its interaction with IL-18 binding protein -
XX PS Example 1; Fig 1B; 23pp; English.
XX CC The present invention relates to mutants of human interleukin-18 (IL-18) protein that have a lower affinity for IL-18 binding protein (IL-18BP) than the wild-type IL-18 protein. The IL-18 mutants of the invention comprise mutations in one or more amino acid residues which are involved in its interaction with IL-18BP. The mutations comprise substitutions, preferably non-conservative, additions or deletions. A pharmaceutical composition comprising an IL-18 mutant is useful for treating a disease which is prevented or alleviated by a T helper type I (Th1) response, including cancer and viral disease. The IL-18 mutants are useful in the treatment of the above diseases, microbial infections, in tumour immunotherapy, and as an adjuvant in DNA vaccination and in graft versus tumour therapy. The IL-18 mutants are resistant to, or less susceptible to, neutralisation than the wild-type protein. The present sequence represents human wild-type mature IL-18 protein.
XX SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 24; Length 157;
Best Local Similarity 99.4%; Pred. NO. 8.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 10

AAV85167
ID AAV85167 standard; Protein; 158 AA.
XX AC AAY85167;
XX 23-JUN-2000 (first entry)
XX Human interleukin-18 (IL-18) amino acid sequence.
DE Interleukin-18; production; IL-18; human; medical injection product.
XX Homo sapiens.
XX CN1243130-A.
XX 02-FEB-2000.
XX 24-JUL-1998; 98CN-0103307.
XX 24-JUL-1998; 98CN-0103307.
XX (WUGG/) WU G.
XX Wu G, Liu Z;
XX WPI; 2000-340020/30.
XX N-PSDB; AAA10526.
XX Preparation method for engineering bacteria for recombination of human
XX interleukin-18 and its product thereof -
XX Claim 1; Page 2; 17pp; English.

XX This sequence represents the human interleukin-18 (IL-18) amino acid
XX sequence. The invention relates to a method for engineering bacterium for
XX recombination of human IL-18 and a method for the preparation of IL-18. A
XX primer containing a restriction endonuclease site can be used to.
XX accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
XX stop codon preferred by coli bacillus to raise the expression rate. The
XX method uses a high-amplification culture medium to increase the
XX expression level and only requires a one-step purification process to
XX obtain a medical injection-pure product.

XX Sequence 158 AA;

Query Match 99.9%; Score 811; DB 21; Length 158;
Best Local Similarity 99.4%; Pred. No. 8.3e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 61

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120
DB 62 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 121

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
DB 122 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 158

RESULT 11

AAW48959
ID AAW48959 standard; Peptide; 180 AA.
XX AC AAW48959;
XX 25-SEP-1998 (first entry)
XX Wild-type human interferon-gamma inducing factor.
XX Interferon-gamma inducing factor; interferon-gamma; killer cell;
XX antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
XX hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
XX osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..23
XX Protein /note= "signal peptide"
XX /note= "Mature human IGIF which is claimed by the
XX inventors under claim 3 in the specification"

EP845530-A2.

03-JUN-1998.

28-NOV-1997; 97EP-0309632.

14-NOV-1997; 97JP-0329715.

29-NOV-1996; 96JP-0330307.

21-JAN-1997; 97JP-0020906.

(HAYE) HAYASHIBARA SEIBUTSU KAGAKU.

Kurimoto M, Okamoto I, Yamamoto K;

WPI; 1998-288747/26.

N-PSDB; AAV32754.

XX Mutants of interferon-gamma inducing polypeptide - useful as
XX antitumour, antiviral, antimicrobial or anti-immunopathic agents

XX Claim 3; pages 36-37; 59pp; English.

XX The present sequence represents the wild-type human interferon-gamma
XX inducing factor (IGIF). The invention provides for mutant human and
XX mouse interferon-gamma inducing factors in which one or more cysteine
XX residues are replaced with different residues at or away from the
XX consensus sequences shown in AAW48956-W48958. The mutant IGIFs are
XX capable of stimulating immunocompetent cells for the production of
XX interferon-gamma and are claimed to be less toxic, more active and
XX stable than the corresponding wild type IGIF. The mutant IGIFs are also
XX claimed to enhance killer cell cytotoxicity and/or induce killer cell
XX formation, and may therefore be useful as antitumour agents, antitumour
XX immunotherapeutics, antiviral agents and antimicrobial agents. The
XX mutant IGIFs are also claimed to be useful for treating hepatitis, solid
XX acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, and
XX malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
XX thrombopenia caused by radiation- and chemo-therapy.

XX Sequence 180 AA;

Query Match 99.9%; Score 811; DB 19; Length 180;
Best Local Similarity 99.4%; Pred. No. 9.9e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

DB 24 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 83

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDKMKQFESSY 120

Db 84 AVTISVCKEKTSTSCENKIIISFKEMNPPDNKOTKSDIIFQRSVPGHDKMQFESSY 143
121 EGYFLACERDLFKLLKKEDELGDRSIMFTVQNE 157
144 EGYFLACERDLFKLLKKEDELGDRSIMFTVQNE 180

RESULT 12
AAW22047
ID AAW22047 standard; Protein; 193 AA.
AC AAW22047;
XX
DT 14-JAN-1998 (first entry)
DE Interferon gamma inducing factor-2 (IGIF-2) protein.
KW Interferon gamma inducing factor-2; IGIF-2; leucocyte; lymphocyte;
KW inflammation; proliferation; differentiation; maturation; tissue damage;
KW human.
OS Homo sapiens.
XX
FN WO9724441-A1.
XX
PD 10-JUL-1997.
XX
PF 20-DEC-1996; 96WO-US04032.
XX
PR 29-DEC-1995; 95US-0580667.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Cocks BG, Coleman R, Hawkins PR;
XX
DR WPI; 1997-363677/33.
DR N-PSDB; AAT74987.
XX
PT Novel interferon gamma inducing factor-2 - used to screen for
PT compounds to diagnose, treat or prevent tissue damage associated
PT with inflammation
XX
PS Claim 1; Page 46; 60pp; English.
XX
CC This is the protein sequence of interferon gamma inducing factor-2
CC (IGIF-2). An IGIF-2 variant (AAW31757) and an IGIF variant (AAW22049),
CC which may be an alternate transcript, also exist. Probes derived from
CC the nucleic acid sequences can be used to quantify the expression of
CC IGIF-2 in conditions that are associated with inflammation or aberrant
CC expression of IGIF-2. The protein can be used to screen for compounds
CC that interact with IGIF-2, such as antibodies, antagonists or other
CC inhibitors (especially ribozymes or antisense sequences) of IGIF-2
CC expression or activity. The protein can also be used to diagnose,
CC prevent or treat IGIF-2 induction of proliferation, differentiation or
CC maturation of leucocytes or lymphocytes, especially in relation to tissue
CC damage associated with inflammation.
XX
SQ Sequence 193 AA;

Query Match 99.9%; Score 811; DB 18; Length 193;
Best Local Similarity 99.4%; Pred. No. 1.1e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96
61 AVTISVCKEKTSTSCENKIIISFKEMNPPDNKOTKSDIIFQRSVPGHDKMQFESSY 120
97 AVTISVCKEKTSTSCENKIIISFKEMNPPDNKOTKSDIIFQRSVPGHDKMQFESSY 156
121 EGYFLACERDLFKLLKKEDELGDRSIMFTVQNE 157

Db 157 EGYFLACERDLFKLLKKEDELGDRSIMFTVQNE 193

RESULT 13
AAW46592
ID AAW46592 standard; Protein; 193 AA.
XX
AC AAW46592;
XX
DT 21-MAY-1998 (first entry)
DE Amino acid sequence of human interleukin-1-gamma.
XX
KW Interleukin-1-gamma; IL-1-gamma; mouse; cytokine; IGIF; interferon-gamma;
KW induction; antibody; diagnostic assay; fusion protein; activity;
KW immunological disorder; allergy.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT /note= "beta-1 region"
FT Region
FT /note= "beta-2 region"
FT Region
FT /note= "beta-3 region"
FT Region
FT /note= "beta-4 region"
FT Region
FT /note= "beta-5 region"
FT Region
FT /note= "beta-6 region"
FT Region
FT /note= "beta-7 region"
FT Region
FT /note= "beta-8 region"
FT Region
FT /note= "beta-9 region"
FT Region
FT /note= "beta-10 region"
FT Region
FT /note= "beta-11 region"
FT Region
FT /note= "beta-12 region"
XX
FN WO9744468-A1.
XX
PD 27-NOV-1997.
XX
PF 16-MAY-1997; 97WO-US07282.
XX
PR 20-MAY-1996; 96US-0651998.
XX (SCHE) SCHERING CORP.
XX Bazan JF, Hardiman GT, Kastelein RA, Sana TR, Timans JC;
XX WPI; 1998-018522/02.
DR N-PSDB; AAV05368.
XX
PT Antagonist of human interleukin-1-gamma - used for treating
PT immunological disorders caused by human IL-1-gamma
XX
PS Disclosure; Pages 54-55; 63pp; English.
XX
CC The present sequence represents human interleukin-1-gamma (IL-1-gamma).
CC The protein is the human equivalent of a mouse cytokine, IGIF, which
CC induces certain T cells to produce interferon-gamma. Human IL-1-gamma
CC and mouse IGIF show 71% identity at the nucleotide level and
CC approximately 68% identity at the amino acid level. Antagonists of
CC IL-1 gamma, e.g. antibodies, can be used in a method for treating a
CC condition caused by human IL-1 gamma. The antibodies can also be used

CC in diagnostic assays. The IL-1-gamma protein can be covalently
CC conjugated to polyethylene glycol or to a polypeptide, and the fusion
CC protein used in a pharmaceutical composition for supplying the
CC biological activity of IL-1 gamma. Conditions that can be treated using
CC the human IL-1-gamma protein include immunological disorders, allergies,
CC and infectious diseases. The IL-1-gamma can also be used to detect the
CC presence of the protein or its receptor.

XX Sequence 193 AA;
SQ Query Match 99.9%; Score 811; DB 19; Length 193;
Best Local Similarity 99.4%; Pred. No. 1.1e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSOPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSOPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKENPPDNIKDTKSDIIFQFORSVPGHDNKMQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKENPPDNIKDTKSDIIFQFORSVPGHDNKMQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 14

AAB30541
ID AAB30541 standard; Protein; 193 AA.

XX AC AAB30541;
XX DT 06-MAR-2001 (first entry)
XX DE A human IL-18 with a caspase-8 cleavage site.
XX KW Protease cleavage site; caspase-1; interleukin-18; IL-18; protease.
XX OS Synthetic.
XX OS Homo sapiens.

XX Key Location/Qualifiers
FH Cleavage-site 33..36
FT /note= "caspase-8 cleavage site"

XX WO200061768-A2.

XX 19-OCT-2000.

XX 13-APR-2000; 2000WO-IL00220.

XX 13-APR-1999; 99IL-0129427.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Rubinstein M, Liu B, Novick D, Dinarello C, Graber P;

XX WPI; 2001-006910/01.

XX N-PSDB; AAC62200.

XX Preparation of biologically active molecules from its inactive
PT precursors, comprises mutating their native cleavage site to a site
PT capable of being cleaved by protease and cleaving the mutated molecule

XX Disclosure; Fig 8a-b; 40pp; English.

XX The present sequence represents a human pro interleukin-18 (IL-18).

XX with a caspase-8 cleavage site. The natural cleavage site of IL-18

XX was mutated to a site susceptible to cleavage by a common protease.

XX The specification describes a method for the preparation of biologically

XX active molecules from their biologically inactive precursors. The method

CC comprises mutating the native cleavage site to a site capable of being
CC cleaved by a protease and cleaving the mutated molecule to yield the
CC active compound. The method is especially used to produce active
CC cytokines, such as IL-18.

XX Sequence 193 AA;

XX Query Match 99.9%; Score 811; DB 22; Length 193;
Best Local Similarity 99.4%; Pred. No. 1.1e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSOPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSOPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKENPPDNIKDTKSDIIFQFORSVPGHDNKMQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKENPPDNIKDTKSDIIFQFORSVPGHDNKMQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 15

AAG63830
ID AAG63830 standard; Protein; 193 AA.

XX AC AAG63830;

XX DT 26-NOV-2001 (first entry)

XX Amino acid sequence of human interleukin 18 (IL-18).

XX T-cell-helper type 2 response; Th2 response; T cell mediated response;

XX allergic response; interleukin 18; IL-18; IGE-mediated allergy;

XX allergic asthma; anaphylactic reaction; asthma associated allergy;

XX IGE dependent allergic rhinoconjunctivitis.

XX Homo sapiens.

XX WO200168896-A1.

XX 20-SEP-2001.

XX 02-MAR-2001; 2001WO-US06869.

XX 10-MAR-2000; 2000US-0188311.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Levy S, Dekruyff RH, Umetsu DT, Maecker H;

XX WPI; 2001-570874/64.

XX N-PSDB; AAH78060.

XX Reducing antigen specific immune response in conditions such as asthma,
PT allergic rhinitis, by reducing a T-cell-helper type 2 T cell mediated
PT antigen-specific allergic response -

XX Disclosure; Page 36; 38pp; English.

XX The specification describes a method for reducing a T-cell-helper

XX type 2 (Th2) T cell mediated antigen-specific allergic response. The

XX method comprises administering a DNA construct encoding a fusion

XX protein of interleukin 18 (IL-18) and an antigen associated with the

XX allergic response. The method is useful for reducing a Th2 T cell

XX mediated antigen-specific allergic response especially IGE-mediated

XX allergic asthma or anaphylactic reactions or IGE dependent allergic

XX rhinoconjunctivitis, and for treating asthma associated allergies where

XX the allergies are ongoing at the time of the administration. The

XX present sequence represents a human IL-18, and is used to construct

XX fusion proteins of the invention.

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XX SQ Sequence 193 AA;
Query Match 99.9%; Score 811; DB 22; Length 193;
Best Local Similarity 99.4%; Pred No. 1,1e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPCHDNKMQFESSY 120
Db 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPCHDNKMQFESSY 156

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193
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Search completed: December 12, 2003, 17:52:26
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: December 12, 2003, 17:41:24 ; Search time 21 Seconds
(without alignments)

316.324 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKXDELGDRSIMFTVQNEED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	811	99.9	157	4	US-09-700-609-1
3	810	99.8	157	2	US-08-896-605A-6
4	810	99.8	157	3	US-08-896-501A-4
5	810	99.8	157	3	US-08-884-324-1
6	810	99.8	157	3	US-08-996-338-26
7	810	99.8	157	3	US-08-558-818-1
8	810	99.8	157	3	US-08-974-469A-1
9	810	99.8	157	3	US-08-832-180-1
10	810	99.8	157	3	US-08-832-198-6
11	810	99.8	157	4	US-09-819-902-6
12	810	99.8	157	4	US-09-752-510-6
13	810	99.8	157	4	US-09-711-899-1
14	810	99.8	157	4	US-09-556-972-26
15	810	99.8	193	2	US-08-896-605A-2
16	810	99.8	193	3	US-08-896-501A-2
17	810	99.8	193	3	US-08-832-180-9
18	801	98.6	157	4	US-08-982-285-6
19	792	97.5	193	4	US-09-597-576-2
20	791	97.4	157	4	US-08-982-285-7
21	791	97.4	157	4	US-08-982-285-8
22	782	96.3	157	4	US-08-982-285-11
23	781	95.2	157	4	US-08-982-285-9
24	772	95.1	157	4	US-08-982-285-12
25	771	95.0	157	4	US-08-982-285-10
26	517	63.7	157	4	US-08-982-285-13
27	515	63.4	157	4	US-08-982-285-5

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Sequence 7, Appli
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Sequence 11, Appli
Sequence 8, Appli
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Sequence 14, Appli
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ALIGNMENTS

RESULT 1
US-08-982-285-4
; Sequence 4, Application US/08982285
; Patent No. 6476197
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Kozi
; APPLICANT: OKAMOTO, Iwao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 7th Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/982,285
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 333,037/96
; FILING DATE: No. 6476197ember 29, 1996
; APPLICATION NUMBER: JP 20,906/97
; FILING DATE: January 21, 1997
; APPLICATION NUMBER: JP 10,053,503
; FILING DATE: No. 6476197ember 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-982-285-4

Query Match 99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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;
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-501A-4
Query Match 99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKEKISXLSCKENKIISFKEMNPPDNKTKSDIIFQRSVPGHDNMQPESSEY 120
Db 61 AVTISVKEKISXLSCKENKIISFKEMNPPDNKTKSDIIFQRSVPGHDNMQPESSEY 120

Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEB 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEB 157

RESULT 5
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takanori OKURA
; APPLICANT: Kakui TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-884-324-1
Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKEKISXLSCKENKIISFKEMNPPDNKTKSDIIFQRSVPGHDNMQPESSEY 120
Db 61 AVTISVKEKISXLSCKENKIISFKEMNPPDNKTKSDIIFQRSVPGHDNMQPESSEY 120

Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEB 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEB 157

RESULT 6
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakui
; APPLICANT: OKURA, Takanori
; APPLICANT: KURIMOTO, Masahi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-DEC-1997
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-996-338-26
Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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61	AVTISVKEKISXLSCEKNIISFKEMPPDNIKTKSDIIFQFQSVPGHDKNQFESSY	120
61	AVTISVKEKISXLSCEKNIISFKEMPPDNIKTKSDIIFQFQSVPGHDKNQFESSY	120
121	EGYFLACKEKRDLPKLIILKKEDELGDRSIMFTVQNE	157
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RESULT 7
 US-08-558-818-1
 ; Sequence 1, Application US/08558818
 ; Patent No. 6197297
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
 ; APPLICANT: KENKYUJO
 ; APPLICANT: KUNIKATA, Toshio
 ; APPLICANT: TANIGUCHI, Mutsuko
 ; APPLICANT: KOHNO, Keizo
 ; APPLICANT: KURIMOTO, Masashi
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
 ; WHICH INDUCES INTERFERON- PRODUCTION

Query Match	99.8%	Score 810;	DB 3;	Length 157;
Best Local Similarity	100.0%;	Pred. No. 4.2e-88;		
Matches 157;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	YFGKLESKLSVIRNLNDQVLFIQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM	60
Db	1	YFGKLESKLSVIRNLNDQVLFIQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM	60
Qy	61	AVTISVKCEKISXLSCENKIISPKEMPPNIIKDTKSDIIFPQRSVGHDKMKQPFESSY	120
Db	61	AVTISVKCEKISXLSCENKIISPKEMPPNIIKDTKSDIIFPQRSVGHDKMKQPFESSY	120

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121 EGYFLACEKRDLPKJLKKEDELGDRSIMFTVQNEED 157
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121 EGYFLACEKRDLPKJLKKEDELGDRSIMFTVQNEED 157

RESULT 8
US-08-974-469A-1
; Sequence 1, Application US/08974469A
; Patent No. 6207641
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: FUKUDA, Shigeharu
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,469A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,879
; FILING DATE:
; APPLICATION NUMBER: JP 78,357/95
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 274,988/95
; FILING DATE: September 29, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-469A-1

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[illegible]

RESULT 9

US-08-832-180-1
; Sequence 1, Application US/08832180
; Patent No. 6214584
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: USHIO, Shimpei
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: OKAMURA, Haruki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832.180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,191
; FILING DATE:
; APPLICATION NUMBER: JP 304,203/94
; FILING DATE: No. 6214584ember 15, 1994
; APPLICATION NUMBER: 10048102
; FILING DATE: September 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: USHIO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-832-180-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKMKOFESSY 120
Db 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKMKOFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 10

US-08-832-198-6
; Sequence 6, Application US/08832198
; Patent No. 6242255
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitaukiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832.198
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP not yet received
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; OTHER INFORMATION: 'Ile' or 'Thr'
; US-08-832-198-6

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKMKOFESSY 120
Db 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKMKOFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 11
US-09-819-902-6
; Sequence 6, Application US/09819902
; Patent No. 6403079
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuakiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/819,902
; FILING DATE: 29-Mar-2001
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/832,798
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'Ile' or 'Thr'
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-819-902-6

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTFIILSMYKDSQPRGM 60
DB 1 YFGKLESKLVIRNLDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTFIILSMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKENPPDNIDKTSDIIFQORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSKENKIISFKENPPDNIDKTSDIIFQORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNEED 157

DB 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNEED 157
RESULT 12
US-09-752-510-6
; Sequence 6, Application US/09752510
; Patent No. 6441138
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuakiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/752,510
; FILING DATE: 03-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: <unknown>
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'Ile' or 'Thr'
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-752-510-6

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTFIILSMYKDSQPRGM 60
DB 1 YFGKLESKLVIRNLDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTFIILSMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKENPPDNIDKTSDIIFQORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSKENKIISFKENPPDNIDKTSDIIFQORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNEED 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 13
US-09-711-899-1
; Sequence 1, Application US/09711899
; Patent No. 6509449
; GENERAL INFORMATION:
; APPLICANT: <Unknown>
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; WHICH INDUCES INTERFERON- PRODUCTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,899
; FILING DATE: 13-NO. 6509449-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,818
; FILING DATE: 2000-11-15
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELIC1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-711-899-1

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQPESSSY 120
Db 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 14
US-09-556-972-26
; Sequence 26, Application US/09556972
; Patent No. 6559298
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; OKURA, Takao
; KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

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Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 15
US-08-896-605A-2
; Sequence 2, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556.972
FILING DATE: 24-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/996.338
FILING DATE: 22-DEC-1997
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-556-972-26

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQPESSSY 120
Db 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-896-605A-2

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Query Match      99.8%; Score 810; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.5e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AVTISVKCEKISXLSKENKIISFKENPPDNIKDTKSDIIFQORSVPGHDNKNQFESSY 120
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QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
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Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193
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Search completed: December 12, 2003, 17:47:03
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
941.917 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDLGDRSIMFTVQNE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues
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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	811	99.9	157	12	US-10-311-491-3 Sequence 3, Appli
4	811	99.9	157	14	US-10-100-057-6 Sequence 6, Appli
5	811	99.9	157	14	US-10-094-153-2 Sequence 2, Appli
6	811	99.9	157	15	US-10-260-576-4 Sequence 4, Appli
7	811	99.9	157	15	US-10-297-136-1 Sequence 1, Appli
8	811	99.9	193	9	US-09-798-075-1 Sequence 1, Appli
9	811	99.9	193	10	US-09-770-528-8 Sequence 8, Appli
10	811	99.9	193	12	US-10-311-491-1 Sequence 1, Appli
11	811	99.9	233	12	US-10-311-491-10 Sequence 10, Appli
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13	810	99.8	157	10	US-09-924-099-21 Sequence 21, Appli
14	810	99.8	157	12	US-10-349-023-26 Sequence 26, Appli
15	810	99.8	157	16	US-10-327-069-1 Sequence 1, Appli

16	807	99.4	157	14	US-10-094-153-10 Sequence 10, Appli
17	807	99.4	193	14	US-10-094-153-9 Sequence 9, Appli
18	805	99.1	157	14	US-10-094-153-6 Sequence 6, Appli
19	805	99.1	157	14	US-10-094-153-7 Sequence 7, Appli
20	805	99.1	193	14	US-10-094-153-3 Sequence 3, Appli
21	805	99.1	193	14	US-10-094-153-4 Sequence 4, Appli
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34	791	97.4	157	15	US-10-260-576-8 Sequence 8, Appli
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36	782	96.3	157	14	US-10-100-057-25 Sequence 25, Appli
37	782	96.3	157	15	US-10-260-576-11 Sequence 11, Appli
38	781	96.2	157	11	US-09-030-061-23 Sequence 23, Appli
39	781	96.2	157	14	US-10-100-057-23 Sequence 23, Appli
40	781	96.2	157	15	US-10-260-576-9 Sequence 9, Appli
41	772	95.1	157	11	US-09-030-061-26 Sequence 26, Appli
42	772	95.1	157	14	US-10-100-057-26 Sequence 26, Appli
43	772	95.1	157	15	US-10-260-576-12 Sequence 12, Appli
44	771	95.0	157	11	US-09-030-061-24 Sequence 24, Appli
45	771	95.0	157	14	US-10-100-057-24 Sequence 24, Appli

ALIGNMENTS

RESULT 1
US-09-775-046-9
; Sequence 9, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-046-9

Query Match	99.9%	Score 811;	DB 10;	Length 157;
Best Local Similarity	99.4%	Pred. No. 2.1e-81;		
Matches 156;	Conservative	0; Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	YFGKLESKLSVIRNLNDQVLPIDQGNRPLEDMTDSCRDNAPRTIIFIISMYKDSQPRGM	60	
Db	1	YFGKLESKLSVIRNLNDQVLPIDQGNRPLEDMTDSCRDNAPRTIIFIISMYKDSQPRGM	60	
Qy	61	AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSIIFFQKSVFCHDNKMQPFESSY	120	
Db	61	AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSIIFFQKSVFCHDNKMQPFESSY	120	
Qy	121	EGYFLACEKERDLPFKILKKEDLGDRSIMFTVQNE	157	
Db	121	EGYFLACEKERDLPFKILKKEDLGDRSIMFTVQNE	157	

RESULT 2
US-09-030-061-6
; Sequence 6, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946Aluyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/030, 061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-030-061-6
Query Match 99.9%; Score 811; DB 11; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGRSINFVTQVNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSINFVTQVNE 157
RESULT 3
US-09-030-061-6
; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDavitt, Damien
Query Match 99.9%; Score 811; DB 11; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGRSINFVTQVNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSINFVTQVNE 157
RESULT 4
US-10-100-057-6
; Sequence 6, Application US/10100057
; Publication No. US20020150555A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; HORWOOD, Nicole Joy
; UDAGAWA, No. US20020150555Aluyuki
; KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/100, 057
; FILING DATE: 19-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/030, 061
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1

; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: Active IL-18 Polypeptide
; CURRENT APPLICATION NUMBER: US/10/311,491
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3
Query Match 99.9%; Score 811; DB 12; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGRSINFVTQVNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSINFVTQVNE 157
RESULT 4
US-10-100-057-6
; Sequence 6, Application US/10100057
; Publication No. US20020150555A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; HORWOOD, Nicole Joy
; UDAGAWA, No. US20020150555Aluyuki
; KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/100, 057
; FILING DATE: 19-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/030, 061
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1


```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-100-057-6

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 5
US-10-094-153-2
; Sequence 2, Application US/10094153
; Publication No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; APPLICANT: Kim, Soo Hyun
; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-153-2

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 6
US-10-260-576-4
; Sequence 4, Application US/10260576
; Publication No. US20030092130A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Kozo
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
```

```

; OKAMOTO, Iwao
; KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 7th Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/260,576
; FILING DATE: 01-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 333,037/96
; FILING DATE: No. US20030092130A1ember 29, 1996
; APPLICATION NUMBER: JP 20,906/97
; FILING DATE: January 21, 1997
; APPLICATION NUMBER: JP 10,053,503
; FILING DATE: No. US20030092130A1ember 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-260-576-4

Query Match          99.9%; Score 811; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 7
US-10-297-136-1
; Sequence 1, Application US/10297136
; Publication No. US20030113292A1
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: TAL-SINGER, RUTH
; APPLICANT: WOODNUTT, GARY
; APPLICANT: CHISARI, FRANCIS V.
; APPLICANT: DILLON, SUSAN B.
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
```

TITLE OF INVENTION: IL-18 and IL-18 Combinations
FILE REFERENCE: P51144
CURRENT APPLICATION NUMBER: US/10/297,136
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/US01/17924
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/208,869
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-10-297-136-1

Query Match 99.9%; Score 811; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISTLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 8

US-09-798-075-1

Sequence 1, Application US/09798075

Patent No. US2001004418A1

GENERAL INFORMATION:

APPLICANT: Levy, Shoshana

APPLICANT: Dekryuff, Rosemarie

APPLICANT: Umetsu, Dale

APPLICANT: Maeker, Holden

TITLE OF INVENTION: Treatment of Allergies

FILE REFERENCE: STAN-179

CURRENT APPLICATION NUMBER: US/09/798,075

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 60/188,311

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 193

TYPE: PRT

ORGANISM: Homo sapiens

US-09-798-075-1

Query Match 99.9%; Score 811; DB 9; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.8e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 9

US-09-770-528-8

Sequence 8, Application US/09770528

Patent No. US2002016432A1

GENERAL INFORMATION:

APPLICANT: Hedrick, Joseph A.

Bazan, Theodore R.

Kastelein, Robert A.

TITLE OF INVENTION: Mammalian Cytokines; Related Reagents

and Methods

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: DNAX Research Institute

STREET: 901 California

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/770,528

FILING DATE: 25-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/130,972

FILING DATE: <Unknown>

APPLICATION NUMBER: US 60/055,111

FILING DATE: 06-AUG-1997

APPLICATION NUMBER: US 09/062,866

FILING DATE: 20-APR-1998

APPLICATION NUMBER: US 09/097,976

FILING DATE: 16-JUN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0725K2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-852-9196

TELEFAX: 650-496-1200

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-770-528-8

Query Match 99.9%; Score 811; DB 10; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.8e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSKCNKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 10

US-10-311-491-1

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; Sequence 1, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-1

Query Match          99.9%; Score 811; DB 12; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.8e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db      37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96

Qy      61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 120
Db      97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 156

Qy      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db      157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 11
US-10-311-491-10
; Sequence 10, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-10

Query Match          99.9%; Score 811; DB 12; Length 233;
Best Local Similarity 99.4%; Pred. No. 3.6e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db      77 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 136

Qy      61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 120
Db      137 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 196

Qy      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db      197 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 233

RESULT 12
US-08-996-140-1
; Sequence 1, Application US/08996140
; Publication No. US20030190318A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: USHIO, Shimpei
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,140
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 356,426/1996
; FILING DATE: 26-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 52,526/1997
; FILING DATE: 21-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 163,490/1997
; FILING DATE: 6-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,490/1997
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-996-140-1
```

Query Match 99.8%; Score 810; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKMFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKMFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157

RESULT 13
US-09-924-099-21
Sequence 21, Application US/09924099
Patent No. US20020128450A1
GENERAL INFORMATION:
APPLICANT: NISHIDA, Yoshihiro
APPLICANT: OKURA, Takanori
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 21
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: (73)
OTHER INFORMATION: "Xaa" means an amino acid of isoleucine or threonine.

US-09-924-099-21

Query Match 99.8%; Score 810; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKMFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKMFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157

RESULT 14
US-10-349-023-26
Sequence 26, Application US/10349023
Publication No. US20030133919A1
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
OKURA, Takanori
KURIMOTO, Masashi

TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/349,023
FILING DATE: 23-Jan-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/556,972
FILING DATE: 24-Apr-2000
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-349-023-26

Query Match 99.8%; Score 810; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.7e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKMFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKMFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157

RESULT 15
US-10-327-069-1
Sequence 1, Application US/10327069
Publication No. US20030129184A1
GENERAL INFORMATION:
APPLICANT: KASHI, KAISHA HAYASHIBARA SEIBUTSU KAGAKU
KENTYUJO
KUNIKATA, Toshio
TANIGUCHI, Mutsuko
KOHNO, Keizo
KURIMOTO, Masashi

TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE

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OM protein - protein search, using sw model

Run on: December 12, 2003, 17:50:55 ; Search time 20 Seconds
(without alignments)
754.924 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLDQVL.....LKKEDELGDRSIMFTVQNE 157
Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515	63.4	192	S60226	cytokine IGIF - mouse
2	85	10.5	381	T40341	hypothetical prote
3	82	10.1	263	T39487	hypothetical prote
4	81.5	10.0	270	S10532	interleukin-1 alph
5	80.5	9.9	866	C71509	probable DNA polym
6	79	9.7	452	D64583	hypothetical prote
7	78.5	9.7	204	T44357	hypothetical prote
8	78	9.6	473	T32038	hypothetical prote
9	77.5	9.5	1251	A36677	neuronal cell cycl
10	77	9.5	364	A81261	probable periplasm
11	76	9.4	632	T00679	hypothetical prote
12	76	9.4	747	E84698	hypothetical prote
13	75.5	9.3	192	S15661	(2'-5')oligo(A) sy
14	75.5	9.3	270	I46620	interleukin-1 alph
15	75.5	9.3	1036	H64245	hypothetical prote
16	75.5	9.3	1663	1 C3MS	complement C3 prec
17	75	9.2	1064	S74450	protein-tyrosine k
18	75	9.2	2470	I50726	cation-independent
19	74.5	9.2	334	T04198	hypothetical prote
20	74.5	9.2	389	B89277	TRK potassium upta
21	74.5	9.2	467	A48713	serine/threonine-s
22	74.5	9.2	1228	A57384	multimerin, endoth
23	74.5	9.2	1510	T16927	hypothetical prote
24	74	9.1	245	B90488	hypothetical prote
25	74	9.1	361	E96904	minD family ATPase
26	74	9.1	376	T24925	hypothetical prote
27	74	9.1	467	2 I49609	proto-oncogene pro
28	74	9.1	467	2 A47388	serine/threonine p
29	74	9.1	680	2 A28121	major merozoite su

30	74	9.1	810	2 B71639	virb4 protein prec
31	74	9.1	1772	2 A45532	major merozoite su
32	73.5	9.1	268	2 H85641	probable small sub
33	73.5	9.1	268	2 C90781	probable small sub
34	73	9.0	418	2 D82932	seryl-tRNA synthet
35	73	9.0	447	2 D26293	hypothetical prote
36	72.5	8.9	268	1 B24073	interleukin-1 alph
37	72.5	8.9	313	2 C96528	protein P27J15.10
38	72.5	8.9	436	2 G97701	polynucleotide ade
39	72.5	8.9	475	2 T32036	hypothetical prote
40	72.5	8.9	888	2 A38539	p101 protein precu
41	72.5	8.9	1246	2 S60954	probable membrane
42	72.5	8.9	1294	2 T48349	EN2 protein - Ara
43	72.5	8.9	1997	2 F71607	DNA helicase II BR
44	72	8.9	264	2 B90051	hypothetical prote
45	72	8.9	1613	2 S39059	protein BRG1 - hum

ALIGNMENTS

RESULT 1

S60226
Cytokine IGIF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S60226
R:Okamura, H.; Teutsui, H.; Komatsu, T.; Yutendo, M.; Hakura, A.; Tanimoto, T.; Torigoe, Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:96061009; PMID:7477296
A:Accession: S60226
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OKA>
A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823
C:Superfamily: Mus musculus cytokine IGIF

Query Match 63.4%; Score 515; DB 2; Length 192;
Best Local Similarity 64.9%; Pred. No. 2.7e-42;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

Qy	2	FGKLESKLSVIRNLDQVLFDIQGNRPLFEDMTDSCRDNAPRTIFITSMYKDSOPRGMA	61
Db	37	FGRHCTTAVIRNINDQVLFVDK-RQVFEDMTDIDQASSEPQTRLIIMYKDSVRCGLA	95
Qy	62	VTISVKCEKISXLSCEKNKIISFKEMNPPDNIKOTKSDIIFQRSVPVGHNNKQFESSSYE	121
Db	96	VTLSVKDSKMSLTSCKNKIISFBEIMPENIDDIQSDLIIPFKRVPGH-NKMBFESSLYE	154
Qy	122	GYFLACKEKRDPLFKLILKKEDELGDRSIMFTVQN	155
Db	155	GHLFLACQKEDDAFKLILKKEDELGDRSIMFTVQN	188

RESULT 2

T40341
hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40341
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M. submitted to the EMBL Data Library, March 1997
A:Reference number: Z21922
A:Accession: T40341
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-381 <WOO>
A:Cross-references: EMBL:AL022070; PIDN:CAA17782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c
A:Experimental source: strain 972h-; cosmid c3B9
C:Genetics:
A:Gene: SPDB:SPBC3B9.02c

RESULT 4
S10532
interleukin-1 alpha precursor - pig
N/Alternate names: hematopoietin-1; IL-1 alpha
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 20-Feb-1995 #sequence_revision 22-Nov-1996 #text_change 28-Jan-2000
C/Accession: S10532
R/Maliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.E.
Nucleic Acids Res. 19, 4282, 1990
A/Title: Porcine IL-1 alpha cDNA nucleotide sequence.
A/Reference number: S10532; MUID: 90332454; PMID: 2377484
A/Accession: S10532
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-270 <NAL>
A/Cross-references: EMBL:X52731; NID:q1987; PID:CAA36945.1; PID:q1988

hypothetical protein HP0508 - *Helicobacter pylori* (strain 26695)
 C:Species: *Helicobacter pylori*
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C:Accession: D64583
 R:Tomb, J.F.; White, O.; Kervatage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodak, A.; McKenna, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frazer, C.
A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: D64583
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-452 <TOW>
A:Cross-references: GB:AE000565; GB:AE000511; NID:g23113616; PIDN:AA007578.1; PID:g2311362

Query Match 9.7%; Score 79; DB 2; Length 452;
Best Local Similarity 23.8%; Pred. No. 7.4;
Matches 40; Conservative 30; Mismatches 72; Indels 26; Gaps 8;
QY 9 LSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTIFIIISMYKDSQPR----- 58
DB 105 LVYFRQFNQA-FLIAPNDELYEQIRATNTDINFISDLYTLFNGFDPKIANLRKACNV 163
QY 59 -GMATVISVCKEIKISLSCEN-KIISFKEMNPPNIDKTKDIIFFQRSVPCHD---NK 112
DB 164 YSVGVIIYVTTNLNLSCESEFLEKREL---DTSGVTKTSTPFFSR-VEGIDAGTLGK 219
QY 113 MQFESSSYEGYF----LACEKERDLFKLILKKEDELGRSIFMTVQNE 156
DB 220 L-FSGSOSKNYFAYVDALVKKEKRVIRKKREKIDSREIKKE 266

RESULT 7
T44357
hypothetical protein [imported] - Clostridium histolyticum
C:Species: Clostridium histolyticum
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
A:Accession: T44357
R:Matsumita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A. J. Bacteriol. 181, 923-933, 1999
A:Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum.
A:Reference number: 222752; MUID:99121032; PMID:9922257
A:Accession: T44357
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-204 <MAT>
A:Cross-references: EMBL:AB014075; NID:g3868863; PIDN:BA34544.1; PID:g3892648
A:Experimental source: strain JCM 1403

Query Match 9.7%; Score 78.5; DB 2; Length 204;
Best Local Similarity 26.4%; Pred. No. 3.2;
Matches 32; Conservative 19; Mismatches 51; Indels 19; Gaps 5;
QY 9 LSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTIFII--SNYKDSQPRGMATISV 66
DB 25 ISTENRNHAKSSNKQGEAKTEKIN-----IDNSNSIKIVYSLKPEGEQNKTTVDE 80
QY 67 KCEK-----ISXLSCKENKIISFKEMNPPNIDKTKDIIFFQRSVPCHDKNQFESS 119
DB 81 CIEKFNKDKKVISDWTKEQVLAFFKCHD--YNLKDIDKQIVFSRSI-----NKYQEGK 134
QY 120 Y 120
DB 135 Y 135

RESULT 8
T32038
hypothetical protein F41B5.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 16-Feb-2001
A:Accession: T32038
R:Dante, M.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F41B5.
A:Reference number: Z21115

A:Accession: T32038
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-473 <DAN>
A:Cross-references: EMBL:AF016676; PIDN:AA025900.1; GSPDB:GN00023; CESP:F41B5.2
A:Experimental source: strain Bristol N2; clone F41B5
C:Genetics:
A:Gene: CESP:F41B5.2
A:Map position: 5
A:Introns: 67/1; 233/2; 403/3
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; iron; metalloprotein
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 9.6%; Score 78; DB 2; Length 473;
Best Local Similarity 21.5%; Pred. No. 9.7;
Matches 32; Conservative 28; Mismatches 57; Indels 32; Gaps 6;
QY 10 SVIRNLNDQVLF---IDQGNRPFLFEDMTSDCDRNAPRTIFIIISMYKDSQPRGMATISV 66
DB 170 NAIANVINQIFGVYFDESQEEYKLLKH-----LIEPQENVTSKATVQV 216
QY 67 KCEKISXLSCKENKIISFKEMNPPNIDKTKDII-FFQRSVPCHDKNQFESSSYEGYFL 125
DB 217 FAPKL-----GKILPGESLE--DLMKDWKNSFYDFNTQIENHRQKIDFDSSESQDYAE 268
QY 126 ACEKERDLFKLILKKEDELGRSIFMTVQ 154
DB 269 AYLKEQ-----KKYEALGDTFLFSNKQ 290

RESULT 9
A56677
neuronal cell cycle withdrawal protein QN1 - quail (fragment)
C:Species: Coturnix coturnix (quail)
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000
A:Accession: A56677
R:Bidou, L.; Crisanti, P.; Blancher, C.; Pessac, B. Mech. Dev. 43, 159-173, 1993
A:Title: A novel cDNA corresponding to transcripts expressed in retina post-mitotic neur
A:Reference number: A56677; MUID:9412859; PMID:8297788
A:Accession: A56677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1251 <BID>
A:Cross-references: GB:S68151; NID:g545153; PIDN:AA014007.1; PID:g4261707
A:Note: conceptual translation not given

Query Match 9.5%; Score 77.5; DB 2; Length 1251;
Best Local Similarity 23.5%; Pred. No. 34;
Matches 38; Conservative 37; Mismatches 64; Indels 23; Gaps 9;
QY 6 ESKLSVI-RNLNDQVLF---DQGNRPFLFEDMTSDCDRNAPRTIFIIISMYKDSQPRGMA 61
DB 648 EEKLAQIQKEMEDQEVIIQGVQGENERLYQMKDLQIQNKQVE---QMYKENQCL-MS 702
QY 62 VTSVKCEKISXLSCKENKIISFKEMNPPNIDKTKDIIFFQRSVPCHDKNQF----- 116
DB 703 ELIALR-EKVERINIQSV--RESEPARN--QSFTELISLRAARKEETKLREIRRLK 757
QY 117 -SSSYEGYFLACEKERDLFKLILKKEDELGRSIFMTVQNE 156
DB 758 QDKQALELDLQAKKERDLAKVQITSTS--SEKSYEFKIMEE 797

RESULT 10
A81261
probable periplasmic protein Cj1643 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
A:Accession: A81261
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: A81261
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <PAR>
A:Cross-references: GB:AL111168; GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73631.1; PID:g696906
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: CJ1643

Query Match 9.5%; Score 77; DB 2; Length 364;
Best Local Similarity 24.8%; Pred. No. 8.9;
Matches 38; Conservative 21; Mismatches 40; Indels 54; Gaps 9;

QY 12 IRLNLDQVLFIDQGNRPLFEDMTDSCRD-NAPRTIFIISMYK---DSQPR-----58
Db 211 LRKLNKILFADRGSTLYFQVLRDN--MDLNISTEVEFADKLSKFNLPDSKPKKITNFTS 268
QY 59 --GMATISVCKEKI-----SXLSCKENII-SPEKNPPDNI-----92
Db 269 NLGLTYNASLVVTKIDPKSKVSNAGFMVGDKILRVNNIILNPKEL---QNILSAGNDPS 325
QY 93 -----KDTKSDIIFQSVPGH-----DNKMQF 115
Db 326 ILIERKSTKLPLSNFNFELGGNANSNGDGKQFP 358

RESULT 11
T00679
hypothetical protein At2g43990 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F6E13.12
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00679; A84873
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Croesby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: T00679
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-632 <ROU>
A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212856
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84873
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-632 <STO>
A:Cross-references: GB:AE002093; NID:g3212856; PIDN:AAC23407.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g43990; F6E13.12
A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 632;
Best Local Similarity 25.8%; Pred. No. 21;
Matches 34; Conservative 29; Mismatches 40; Indels 30; Gaps 9;

QY 28 PLFEDMTDSD-CRDNAPRTIFIISMYKDSQPRGMVATISVKCEK-----ISXLSCKENK 79
Db 368 PLSDRSASDCLNWSGRSLSPMDIYKETRR---ISSLSNPNLFRFRFHLSCDGE 424
QY 80 IISFK-----EMNPPNIIKDTSDIIFQSVPGH-----BSSYEGYF-LACBK 129
Db 425 ASAFDTSPTCELDPSHLKGDKSSPL-----SVDTLGSENVITQTPESNSSFDNFGILSCSQ 480

QY 130 ERDLFKLILKKED 142
Db 481 AE-----IQKKHD 488

RESULT 12
E84698
hypothetical protein At2g29620 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
A:Accession: E84698
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84698
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-747 <STO>
A:Cross-references: GB:AE002093; NID:g3582336; PIDN:AAC35233.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g29620
A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 747;
Best Local Similarity 24.7%; Pred. No. 26;
Matches 36; Conservative 29; Mismatches 59; Indels 22; Gaps 7;

QY 4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMVAT 63
Db 102 KUKHQOSVVRNARRKV-----EVGKDWDSQASEDERGKVLTLLTGEVLPE---T 150
QY 64 ISVCKEKISXLSCKENKIISFKEMNPPDNIKDTSDIIFQSVPGHDKNQMF---SS 118
Db 151 ITPDMKFKP---RERTLLVAEENVFDSVLDNRDLVELERLISVDG-DDESEVECSSS 205
QY 119 SYEGYFLACEKRDLPKLLK-KEDE 143
Db 206 SSEGEKEEEREDVSKVVAVWTEDD 231

RESULT 13
S15661
(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 16-Jul-1999
C:Accession: S15661; S19108
R:Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G. Nucleic Acids Res. 19, 1917-1924, 1991
A:Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked ge A:Reference number: S15660; MUID:91232962; PMID:1709495
A:Accession: S15661
A:Molecule type: mRNA
A:Residues: 1-192 <RUT>
A:Cross-references: EMBL:X55982
R:Williams, B.
submitted to the EMBL Data Library, September 1990
A:Reference number: S19108
A:Accession: S19108
A:Molecule type: mRNA
A:Residues: 1-175, 'L', 177-192 <WIL>
A:Cross-references: EMBL:X55982; NID:g49714; PIDN:CAA39455.1; PID:g49715
C:Superfamily: oligo(A) synthetase
C:Keywords: nucleotidyltransferase

Query Match 9.3%; Score 75.5; DB 2; Length 192;
Best Local Similarity 23.2%; Pred. No. 5.8;
Matches 42; Conservative 24; Mismatches 50; Indels 65; Gaps 9;

QY 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKD 54

Db 11 GRSDADLVVFNLTSPDQLNQGVLIKEIKQLCEVQHERRC----- 54
Qy 55 SQPRGMVAVTSVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDII----- 100
Db 55 -----GVKFEVSLRSPNRSALSK-LSAPDLLKEVDFVLPAYDLLDHLNLUKK 103
Qy 101 ----FFQR---SVP-GHDNKNQFESSYEGYFLACE--KERDLFKLI-----LKKEDELG 145
Db 104 PNOQFYANLISGVPAKGEGKLSICPMGLQKYFLNCRPTKRLRLRLVTHWYQLCKE-KLG 162
Qy 146 D 146
Db 163 D 163

RESULT 14

I46620

interleukin-1 alpha precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 04-Feb-2000

C:Accession: I46620

R:Maliszewski, C.

Nucleic Acids Res. 14, 4282, 1990

A:Title: Nucleotide sequence of porcine interleukin-1 alpha.

A:Reference number: I46620

A:Accession: I46620

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-270 <MAL>

A:Cross-references: GB:M86730; NID:g164622; PIDN:AAA73198.1; PID:g164623

C:Superfamily: interleukin-1

C:Keywords: lipoprotein; myristylation

F:1-112/Domain: propeptide #status predicted <PRO>

F:113-270/Product: interleukin-1 alpha #status predicted <ILL>

F:82,83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 9.3%; Score 75.5; DB 2; Length 270;
Best Local Similarity 22.0%; Pred. No. 8.7;
Matches 29; Conservative 32; Mismatches 58; Indels 13; Gaps 6;

Qy 8 KLSVIRNLNDQVLFDQGNRPLFEDMTD-----SDCRDNAPRTI-FIISMYKDSQPRGMNAV 62

Db 123 KYNFMRVINHOCILNDARNQSIIRDPSGQYLMAAVLNNLDEAVKFDMAAYTSNDDSQLPV 182

Qy 63 TISVKCEKISXLSCEN--KIISFKEM-NPPDNIKDTKSDIIFORSVPGHDNKNQFSSSS 119

Db 183 TLRIIS-ETRLFVSAQNEDEPVLKELPETPTKTKIDETSLFFWEK----HGNMDYFKSAA 237

Qy 120 YEGYFLACEKER 131

Db 238 HPKLLIATRQEK 249

RESULT 15

H64245

hypothetical protein MG414 - Mycoplasma genitalium

C:Species: Mycoplasma genitalium

C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 02-Mar-2001

C:Accession: H64245; G64245

R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M.; Fuhrmann, J.; Nguyen, D.; Uitterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

C.A.; Venter, J.C.

Science 270, 397-403, 1995

A:Title: The minimal gene complement of Mycoplasma genitalium.

A:Reference number: A64200; MUID:96026346; PMID:7569993

A:Accession: H64245

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1036 <TIGR>

A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046129; TIGR:MG414

A:Experimental source: strain G-37

A:Accession: G64245

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 'M', 310-1036 <TIG2>
A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046128; TIGR:MG413
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
A:Start codon: GTG
C:Superfamily: hypothetical protein MG413

Query Match 9.3%; Score 75.5; DB 2; Length 1036;

Best Local Similarity 21.9%; Pred. No. 43;

Matches 33; Conservative 32; Mismatches 65; Indels 21; Gaps 6;

Qy 14 NLNDQVLFDQGNRPLFED--MTSDCRDNAPRTIIFIISMYKDSQPRGMNAVTSVKCEK- 70

Db 845 SLNDEQLLVKLNITLSEKRLQTTKTVRFNLKNKFINHLVENKQNLVFDVDRSKKL 904

Qy 71 -ISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKNQFSSSSYEGYFLACEK 129

Db 905 FIKGVNNDNQVFSISY-----DLKITNNQTLIV-DANGFDNSIWFDTIS-----EN 950

Qy 130 ERDLFKLI---LKKEDLGRSIMPFTVQNEED 157

Db 951 QTQLFKALSPYLKQNNLQPKRVPDFNLKSOD 981

Search completed: December 12, 2003, 17:54:16

Job time : 21 secs

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